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(54) **Title:** METHODS AND REAGENTS FOR REGULATING BONE AND CARTILAGE FORMATION

(57) **Abstract:** The invention provides methods and compositions for diagnostic assays for detecting bone and cartilage formation and therapeutic methods and compositions for treating disease and disorders related to bone and cartilage formation or resorption, such as osteoporosis and bone fractions. The invention also provides therapeutic methods for diseases related to bone or cartilage formation or resorption. Methods for identifying therapeutics for such diseases are also provided.

METHODS AND COMPOSITIONS FOR REGULATING BONE AND CARTILAGE FORMATION

Background of the Invention

Bone formation is an essential process in embryonic development and plays a critical role in many diseases and conditions which affect millions of humans. For example, osteoporosis is a debilitating disease characterized by excessive bone loss that affects approximately 14 million Americans and costs the U.S. health care system nearly $10 billion annually. In about 40 percent of women and 13 percent of men over 50, osteoporosis is the underlying cause of most hip, spine, and wrist fractures. Recent studies estimate that as much as 70 percent of the variation in bone density is inherited. Bone density reaches adult levels at approximately 18-22 years of life and remains relatively stable until middle age. Loss of bone density in the elderly is the consequence of known factors such as menopause, inadequate nutrition, specific medical conditions, and unknown factors such as a person's genetic constitution. Physicians have very few available drugs to treat declining bone density and need drugs that will promote bone formation in patients.

Bone is continuously remodeled through a coupled process of bone resorption and bone formation. During bone resorption, osteoclasts attach to the mineralized bone matrix and excavate small pits on the bone surface, releasing bone collagen and minerals in the circulation. Subsequently, cross-linked N-telopeptides are released into the bloodstream during osteoclastic activity. During bone formation, osteoblasts are recruited to the newly resorbed areas on the bone where they deposit new collagen. When resorption and formation are in balance, there is no net change in bone mass. After a resting phase during which the bone is mineralized, the remodeling cycle begins again.

In addition to bone formation, another important role for osteoprogenitor cells is in vascular calcification (*see, e.g.* Curr Opin Nephrol Hypertens (2000) 9: 11-15). Calcification is a component of vascular disease that usually occurs in concert with atheroma formation but through distinct pathophysiological processes. Vessel wall osteoprogenitor cells known as calcifying vascular cells can form bone matrix proteins and calcified nodules, analogous to osteoblastic differentiation in bone. These cells have been isolated from the tunica media of bovine and human arteries, and both in-vitro tissue culture models and mouse models of vascular calcification have been established. Studies of the

effects of diabetes mellitus, hyperlipidemia, estrogens and glucocorticoids on calcifying vascular cell function provide insight into the relationship between common human disease states and vascular calcification.

While endochondral bone formation has been fairly well characterized from a morphological perspective, this process remains largely undefined at a gene transcriptional level. *In vitro* and in vivo studies have suggested that bone morphogenetic protein-2 (BMP-2) plays an important role in bone formation, however a detailed understanding of the molecular mechanisms involved would be useful to identify potential genetic targets for controlling bone formation. Accordingly, an understanding of the biochemical and molecular events underlying bone formation, and in particular the identity of the gene(s) expressed during bone and cartilage formation, would provide significant diagnostic and therapeutic applications for the treatment of diseases relating to bone and cartilage formation or resorption, such as osteoporosis, bone fractures and rheumatoid arthritis.

Summary of the Invention

In one embodiment, the invention provides computer-readable media comprising a plurality of digitally encoded values representing the levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 during bone or cartilage formation. The computer-readable medium may comprise values representing levels of expression of at least 5 genes listed in Table 1, 2, 5 and/or 6. The computer-readable medium may comprise values representing levels of expression of CLF-1 and MMP23 during bone or cartilage formation. The computer-readable medium may comprise values representing levels of expression of a plurality of genes listed in Table 6. The computer-readable medium may further comprise at least one value representing a level of expression of at least one gene that is up-or down-regulated during bone or cartilage formation in a precursor cell. The values on the computer-readable medium may represent ratios of, or differences between, a level of expression of a gene in one sample and the level of expression of the gene in another sample. In certain embodiments, less than about 50% of the values in the computer-readable medium represent expression levels of genes which are not listed in Table 1, 2, 5 and/or 6.

In another embodiment, the invention provides computer systems, comprising, e.g., a database comprising values representing expression levels of a plurality of genes listed in

Table 1, 2, 5 and/or 6 during bone or cartilage formation; and, a processor having instructions to, receive at least one query value representing at least one level of expression of at least one gene listed in Table 1, 2, 5 and/or 6; and, compare the at least one query value and the at least one database value. The query value may represent the level of expression of a gene listed in Table 1, 2, 5 and/or 6 in a diseased cell of a subject having or susceptible of having a disease selected from the group consisting of osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; periondontal disease; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss caused by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone fractures.

The invention further provides computer programs for analyzing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a cell, the computer program being disposed on a computer readable medium and including instructions for causing a processor to: receive query values representing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a query cell, and, compare the query values with levels of expression of the plurality of genes listed in Table 1, 2, 5 and/or 6 in a reference cell.

Also provided by the invention are compositions comprising a plurality of detection agents of genes listed in Table 1, 2, 5 and/or 6, which detection agents are capable of detecting the expression of the genes or the polypeptides encoded by the genes, and wherein, e.g., less than about 50% of the detection agents are of genes which are not listed in Table 1, 2, 5 and/or 6. The composition may comprise detection agents of CLF-1 or MMP23. The detection agents may be isolated nucleic acids that hybridize specifically to nucleic acids corresponding to the genes, e.g., at least about 5, 10 or 100 genes of Table 6. Other compositions comprise a plurality of antagonists of a plurality of genes listed in Table 1, 2, 5 and/or 6, e.g., antisense nucleic acids, siRNAs, ribozymes or dominant negative mutants. Yet other compositions comprise a plurality of agonists of a plurality of genes listed in Table 1, 2, 5 and/or 6.

Also within the scope of the invention are solid surfaces to which are linked a plurality of detection agents of genes which are listed in Table 1, 2, 5 and/or 6, which detection agents are capable of detecting the expression of the genes or the polypeptides

encoded by the genes, and wherein, e.g., less than about 50% of the detection agents are not detecting genes listed in Table 1, 2, 5 and/or 6. The detection agents may be isolated nucleic acids that hybridize specifically to the genes. The detection agents may be covalently linked to the solid surface.

Also provided are methods for determining the difference between levels of expression of a plurality of genes in Table 1, 2, 5 and/or 6 in a cell and reference levels of expression of the genes, comprising, e.g., providing RNA from the cell; determining levels of RNA of a plurality of genes listed in Table 1, 2, 5 and/or 6 to obtain the levels of expression of the plurality of genes in the cell; and comparing the levels of expression of the plurality of genes in the cell to a set of reference levels of expression of the genes, to thereby determine the difference between levels of expression of the plurality of genes listed in Table 1, 2, 5 and/or 6 in the cell and reference levels of expression of the genes. The set of reference levels of expression may include the levels of expression of the genes during bone or cartilage formation. The set of reference levels of expression may further include the levels of expression of the genes in a precursor cell. The cell may be a cell of a subject having or susceptible of having a disease selected from the group consisting of osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; periondontal disease; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss caused by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone fractures. The method may comprise incubating a nucleic acid sample derived from the RNA of the cell of the subject with nucleic acids corresponding to the genes, under conditions wherein two complementary nucleic acids hybridize to each other. The nucleic acids corresponding to the genes may be attached to a solid surface. The method may comprise entering the levels of expression of the plurality of genes into a computer that comprises a memory with values representing the set of reference levels of expression. Comparing the level may comprise providing to the computer instructions to perform.

In another embodiment, the invention provides methods for determining whether a subject has or is likely to develop a disease related to bone or cartilage resorption, comprising, e.g., obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression

during normal bone and cartilage formation, wherein significant differences in the levels of expression of the plurality of genes indicates that the subject has or is likely to develop a disease related to bone or cartilage resorption. The disease may be selected from the group consisting of osteoporosis, osteopenia, periondontal disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss caused by an inflammatory disease, rheumatoid arthritis and osteoarthritis.

In another embodiment, the invention provides methods for determining whether a subject has or is likely to develop a disease related to bone or cartilage formation, comprising, e.g., obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant similarities in the levels of expression of the plurality of genes indicates that the subject has or is likely to develop a disease related to bone or cartilage formation. The disease may be selected from the group consisting of osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoma and osteoblastoma, hyperparathyroidism; hypercalcemia of malignancy; and Paget's disease.

In yet another embodiment, the invention provides methods for determining the effectiveness of a treatment intended to stimulate bone or cartilage formation, comprising, e.g., obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant similarities in the levels of expression of the plurality of genes indicates that the treatment is effective. The biological sample may be obtained from the healing region of a bone fracture and a similarity in levels of expression of the plurality of genes in the cell of the subject and the reference levels of expression indicates that the fracture is healing. The method may further comprise iteratively providing a biological sample from the subject, such as to determine an evolution of the levels of expression of the genes in the subject. The set of reference levels of expression may be in the form of a database. The database may be included in a computer-readable medium. The database may be in communications with a microprocessor and microprocessor instructions for providing a user interface to receive expression level data of a subject and to compare the expression level data with the database.

The invention also provides methods for determining the effectiveness of a treatment intended to reduce bone or cartilage formation, comprising, e.g., obtaining a

biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant differences in the levels of expression of the plurality of genes indicates that the treatment is effective.

The methods of the invention may comprise obtaining a patient sample from a caregiver; identifying expression levels of a plurality of genes listed in Table 1, 2, 5 and/or 6 from the patient sample; determining whether the levels of expression of the genes in the patient sample are more similar to those of a cell differentiating into bone or cartilage or to those of a precursor cell; and transmitting the results to the caregiver. The results may be transmitted across a network.

The invention also provides methods for identifying a compound for treating a disease related to bone or cartilage formation, comprising, e.g., providing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a cell of a subject incubated with a test compound; providing levels of expression of a cell differentiating into bone or cartilage; and comparing the two levels of expression, wherein significantly different levels of expression in the two cells indicates that the compound is likely to be effective for treating a disease related to bone or cartilage formation. Also provided are methods for identifying a compound for treating a disease related to bone or cartilage resorption, comprising, e.g., providing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a cell of a subject incubated with a test compound; providing levels of expression of a cell differentiating into bone or cartilage; and comparing the two levels of expression, wherein significantly similar levels of expression in the two cells indicates that the compound is likely to be effective for treating a disease related to bone or cartilage formation.

In yet another embodiment, the invention provides a method for identifying a compound that modulates bone or cartilage formation, comprising, e.g., contacting a mesenchymal precursor cell with an agent that stimulates bone or cartilage formation and a test compound; and determining the level of expression of one or more genes of Tables 1, 2, 6 and 7 during the bone or cartilage formation; wherein a significant similarity or difference between the expression level of the genes in the cell and reference expression levels of the genes during bone or cartilage formation indicates that the test compound modulates bone or cartilage formation. The reference expression levels may be essentially identical to the levels set forth in Table 1, 2, 5 and/or 6. Other methods for identifying a compound that

stimulates bone or cartilage formation, comprises, e.g., contacting a mesenchymal precursor cell with a test compound; and determining the level of expression of one or more genes of Tables 1, 2, 6 and 7 in the cell over time; wherein a similarity between the expression level of the genes in the cell and reference expression levels of the genes during bone or cartilage formation indicates that the test compound stimulates bone or cartilage formation. The reference expression levels may be levels set forth in Table 1, 2, 5 and/or 6.

Also provided are methods for identifying a compound that binds to a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6, comprising, e.g., contacting a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6 with a test compound under essentially physiological conditions; and determining whether the compound binds to the polypeptide. In another embodiment, the invention provides a method for identifying a compound that modulates a biological activity of a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6, comprising, e.g., contacting a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6 with a test compound under essentially physiological conditions; and determining the biological activity of the polypeptide, wherein a higher or lower biological activity of the polypeptide in the presence of the test compound relative to the absence of the test compound indicates that the test compound modulates the biological activity of the polypeptide. The gene may be CLF-1 or MMP23. Other methods for identifying a compound for treating a disease related to bone or cartilage formation or resorption, comprise, e.g., identifying a compound that modulates the activity of a polypeptide encoded by a gene listed in Table 1, 2, 6 or 7; and contacting a mesenchymal precursor cell with the compound in the presence or absence of an agent that stimulates the differentiation into bone or cartilage, wherein stimulation or inhibition of bone or cartilage formation from the mesenchymal cell indicates that the test compound is effective for treating a disease related to bone or cartilage formation or resorption.

The invention also provides methods of treatment, e.g., methods for treating a disease related to bone or cartilage formation or resorption, comprising administering to a subject having a disease related to bone or cartilage formation or resorption a compound that modulates the biological activity of a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6 and thereby modulates bone or cartilage formation, to thereby treat the disease in the subject.

Also within the scope of the invention are diagnostic or drug discovery kits, e.g., comprising a computer-readable medium, a composition a solid surface as described herein, and optionally instructions for use.

Brief Description of the Figures

Figure 1 shows a time course for BMP-2 induction of cytokine receptor-like factor 1 expression (CLF-1) in a mouse model of ectopic bone formation.

Figure 2 shows a time course for BMP-2 induction of matrix metalloproteinase 23 expression (MMP23) in a mouse model of ectopic bone formation.

Detailed Description of the Invention

The invention is based at least in part on the identification of genes which are up- and down-regulated during bone and cartilage formation, in particular, during endochondral or ectopic bone formation. Genes which are modulated include cell surface proteins, cytokines, extracellular matrix proteins, extracellular proteins, intracellular proteins, proteases, receptors, signal transduction proteins and transcription factors. In these expression profiles, certain genes are significantly up-regulated, e.g., MMP23, CLF-1, cadherin 11, and CD68 antigen, and certain genes are significantly down-regulated, e.g., vascular endothelial growth factor B and fatty acid synthase, during differentiation. Tables 1 and 2 list genes which are modulated by a factor of at least about 2 and Tables 5 and 6 list genes which are modulated by a factor of at least about 4. Genes of particular interest are indicated in italics and in bold in the Tables.

Whereas some of the genes listed in the Tables may have been known to be potentially involved in bone and cartilage formation, many other genes listed in the Tables have never before been associated with these processes.

One of the genes not previously known to be associated with bone or cartilage formation that was found to be significantly up-regulated and then down-regulated during the mesenchymal cell differentiation into bone and cartilage is Cytokine Receptor-Like Factor 1 (CLF-1 or CLRF-1) (*see*, Fig. 1). Its up-regulation during bone formation is shown in Fig. 1. The mouse CLF-1 gene (also known as CRLM3 mRNA for cytokine receptor like molecule 3) is transcribed into a 1646 bp mRNA (SEQ ID NO: 1; GenBank Accession No. AB040038) which encodes a mouse protein of 425 amino acids (GenBank Accession No. BAA92777) and a human protein of 422 amino acids. The nucleotide and

amino acid sequences of human CLF-1 are set forth as GenBank Accession Nos. NM_004750 (SEQ ID NO: 1) and NP_004741 (SEQ ID NO: 2) (Elson et al. (1998) J. Immunol. 161:1371. Other human nucleotide sequences have GenBank Accession Nos. AX205046 and AF073515. Other human amino acid sequences have GenBank Accession Nos. AAD39681. The protein is secreted and dimerizes with cardiotrophin-like cytokine (CLC) (Elson et al. (2000) Nature Neuroscience 3(9): 867-872). This heterodimer is also a cytokine (Elson, et al. Nature Neuroscience 3(9):867-872, 2000). The CLC/CLF-1 heterodimeric cytokine binds to ciliary neurotrophic factor receptor (CNTFR) (Elson, et al. Nature Neuroscience 3(9):867-872, 2000). Ligation of CNTFR activates STAT3 (Lelievre et al., J. Biol. Chem. 276(25):22476-22484, 2001). STAT3 activation is tied to the differentiation of a number of cell types such as osteoblasts and osteoclasts. CLF-1 plays a role in promoting the differentiation of mesenchymal progenitor cells towards either chrondrocytes or osteoblasts.

Another gene that was not previously known to be associated with bone or cartilage formation that was found to be up- and then down-regulated during bone and cartilage formation is Matrix Metalloproteinase 23 (MMP23) (*see* Fig. 2). Its upregulation during bone development is set forth in Fig. 2. The gene is transcribed into a mRNA of 1434 base pairs (GenBank Accession No. AF085742), which encodes a protein of 391 amino acid (GenBank Accession No. AAC34886). The nucleotide and amino acid sequences of human MMP23 have GenBank Accession No. AJ005256 (SEQ ID NO: 3) and CAB38176 (SEQ ID NO: 4) (Velasco et al. (1999) J. Biol. Chem. 274:4570. The MMP23 protein is a secreted and also membrane bound protease. Unlike other MMPs it is secreted as an active protease. MMP23 plays a role in normal tissue remodeling (which is part of the bone formation) and in pathological erosion of extracellular matrix proteins (which is part of an arthritic disease).

Although at least some of the genes listed in Tables 1, 2, 5 and/or 6 may not be human genes, corresponding human genes are available or can be obtained within undue experimentation by a person of skill in the art. Methods of the invention may use human or non-human genes, depending on the similarity between the two and the particular use of the genes. A person of skill in the art can determine whether a nucleic acid or protein of a human or non-human gene can be used.

1. Definitions:

As used herein, the following terms and phrases shall have the meanings set forth below. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

The singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise.

The phrase "a corresponding normal cell of" or "normal cell corresponding to" or "normal counterpart cell of" a diseased cell refers to a normal cell of the same type as that of the diseased cell.

The term "agonist," as used herein, is meant to refer to an agent that mimics or up-regulates (e.g., potentiates or supplements) the bioactivity of a protein. An agonist can be a wild-type protein or derivative thereof having at least one bioactivity of the wild-type protein. An agonist can also be a compound that upregulates expression of a gene or which increases at least one bioactivity of a protein. An agonist can also be a compound which increases the interaction of a polypeptide with another molecule, e.g., a target peptide or nucleic acid.

"Antagonist" as used herein is meant to refer to an agent that downregulates (e.g., suppresses or inhibits) at least one bioactivity of a protein. An antagonist can be a compound which inhibits or decreases the interaction between a protein and another molecule, e.g., a target peptide or enzyme substrate. An antagonist can also be a compound that down-regulates expression of a gene or which reduces the amount of expressed protein present.

By "array" or "matrix" is meant an arrangement of addressable locations or "addresses" on a device. The locations can be arranged in two dimensional arrays, three-dimensional arrays, or other matrix formats. The number of locations can range from several to at least hundreds of thousands. Most importantly, each location represents a totally independent reaction site. A "nucleic acid array" refers to an array containing nucleic acid probes, such as oligonucleotides or larger portions of genes. The nucleic acid on the array is preferably single stranded. Arrays wherein the probes are oligonucleotides are referred to as "oligonucleotide arrays" or "oligonucleotide chips." A "microarray," also referred to herein as a "biochip" or "biological chip" is an array of regions having a density of discrete regions of at least about 100/cm^2, and preferably at least about 1000/cm^2. The

regions in a microarray have typical dimensions, e.g., diameters, in the range of between about 10-250 μm, and are separated from other regions in the array by about the same distance.

The term "biological sample", as used herein, refers to a sample obtained from a subject, e.g., a human or from components (e.g., tissues) of a subject. The sample may be of any biological tissue or fluid. Frequently the sample will be a "clinical sample" which is a sample derived from a patient. Such samples include, but are not limited to bodily fluids which may or may not contain cells, e.g., blood, synovial fluid; tissue or fine needle biopsy samples, such as from bone, cartilage or tissues containing mesenchymal cells. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes.

The term "biomarker" of a disease related to bone or cartilage formation or resorption refers to a gene which is up- or down-regulated in a diseased cell of a subject having such a disease, relative to a counterpart normal cell, which gene is sufficiently specific to the diseased cell that it can be used, optionally with other genes, to identify or detect the disease. Generally, a biomarker is a gene that is characteristic of the disease.

"Bone formation" or "bone development" refers to ossification or osteogenesis, such as by endochondral bone formation or intramembraneous bone formation. In intramembraneous bone formation, osteogenesis occurs directly in the condensed mesenchymal cells. In endochondral ossification, mesenchymal cells first condense to form a cartilage model, and then bone formation occurs replacing the cartilage. Osteoprogenitor cells include mesenchymal and skeletal mesenchymal cells. Angiogenesis is part of bone formation. Thus, inhibiting or stimulating angiogenesis may inhibit or stimulate bone formation.

A "cell characteristic of a disease" also referred to as a "diseased cell" refers to a cell of a subject having a disease, which cell is affected by the disease, and is therefore different from the corresponding cell in a non-diseased subject. A diseased cell can also be a cell that is present in significantly higher or lower numbers in a subject having the disease relative to a healthy subject. For example a cell characteristic of cancer is a cancer cell or tumor cell. A diseased cell may also differ from a normal cell in its gene expression profile. A disease cell of a disease relating to bone or cartilage formation or resorption can be a mesenchymal cell, a chondroblast, a chondrocyte, an osteoblast, an osteocyte, a fibroblast or other cells present in bone or cartilage or in bone or cartilage forming tissues.

A "cell sample characteristic of a disease" or a "tissue sample characteristic of a disease" refers to a sample of cells, such as a tissue, that contains at least one cell characteristic of the disease.

A "computer readable medium" is any medium that can be used to store data which can be accessed by a computer. Exemplary media include: magnetic storage media, such as a diskettes, hard drives, and magnetic tape; optical storage media such as CD-ROMs; electrical storage media such as RAM and ROM; and hybrids of these media, such as magnetic/optical storage medium.

The term "derivative" refers to the chemical modification of a compound, e.g., a polypeptide, or a polynucleotide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide can be one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A disease, disorder, or condition "associated with" or "characterized by" or "relating to bone or cartilage formation or resorption" refers to a disease, condition or disorder involving cells that are associated with bone or cartilage formation or resorption. Exemplary diseases include osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; periondontal disease; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss cause by an inflammatory disease, e.g., rheumatoid arthritis and osteoarthritis; wound healing and related tissue repair (e.g., burns, incisions and ulcers) and bone fractures. A "disease relating to bone or cartilage formation" refers to a disease, disorder or condition that can be treated by inhibiting bone or cartilage formation. A "disease relating to bone or cartilage resorption" refers to a disease, disorder or condition that can be treated by stimulating bone or cartilage formation.

A "detection agent of a gene" refers to an agent that can be used to specifically detect a gene or other biological molecule relating to it, e.g., RNA transcribed from the gene and polypeptides encoded by the gene. Exemplary detection agents are nucleic acid probes which hybridize to nucleic acids corresponding to the gene and antibodies.

The term "equivalent" is understood to include nucleotide sequences encoding functionally equivalent polypeptides. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants; and will, therefore, include sequences that differ from the nucleotide sequence of the nucleic acids referred to in Any of Tables 1-5 due to the degeneracy of the genetic code.

The term "expression profile," which is used interchangeably herein with "gene expression profile," "finger print" and "expression pattern" refers to a set of values representing the activity of about 10 or more genes. An expression profile preferably comprises values representing expression levels of at least about 20 genes, preferably at least about 30, 50, 100, 200 or more genes.

"Genes that are up- or down-regulated" in a particular process, e.g., bone and cartilage formation, refer to genes which are up- or down-regulated by, e.g., a factor of at least about 1.1 fold, 1.25 fold, 1.5 fold, 2 fold, 5 fold, 10 fold or more. Exemplary genes that are up- or down-regulated during bone and cartilage formation are set forth in Tables 1, 2, 5 and/or 6. "Genes that are up- or down-regulated in a disease" refer to the genes which are up- or down-regulated by, e.g., at least about 1.1 fold, 1.25 fold, 1.5 fold, 2 fold, 5 fold, 10 fold or more in at least about 50%, preferably 60%, 70%, 80%, or 90% of the patients having the disease.

"Hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing. Two single-stranded nucleic acids "hybridize" when they form a double-stranded duplex. The region of double-strandedness can include the full-length of one or both of the single-stranded nucleic acids, or all of one single stranded nucleic acid and a subsequence of the other single stranded nucleic acid, or the region of double-strandedness can include a subsequence of each nucleic acid. Hybridization also includes the formation of duplexes which contain certain mismatches, provided that the two strands are still forming a double stranded helix. "Stringent hybridization conditions" refers to hybridization conditions resulting in essentially specific hybridization.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral

material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

As used herein, the terms "label" and "detectable label" refer to a molecule capable of detection, including, but not limited to, radioactive isotopes, fluorophores, chemiluminescent moieties, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, dyes, metal ions, ligands (e.g., biotin or haptens) and the like. The term "fluorescer" refers to a substance or a portion thereof which is capable of exhibiting fluorescence in the detectable range. Particular examples of labels which may be used under the invention include fluorescein, rhodamine, dansyl, umbelliferone, Texas red, luminol, NADPH, alpha - beta -galactosidase and horseradish peroxidase.

The "level of expression of a gene" refers to the activity of a gene, which can be indicated by the level of mRNA, as well as pre-mRNA nascent transcript(s), transcript processing intermediates, mature mRNA(s) and degradation products, and polypeptides encoded by the gene. Accordingly, the level of expression of a gene also refers to the amount of polypeptide encoded by the gene.

The phrase "normalizing expression of a gene" in a diseased cell refers to an action to compensate for the altered expression of the gene in the diseased cell, so that it is essentially expressed at the same level as in the corresponding non diseased cell. For example, where the gene is over-expressed in the diseased cell, normalization of its expression in the diseased cell refers to treating the diseased cell in such a way that its expression becomes essentially the same as the expression in the counterpart normal cell. "Normalization" preferably brings the level of expression to within approximately a 50% difference in expression, more preferably to within approximately a 25%, and even more preferably 10% difference in expression. The required level of closeness in expression will depend on the particular gene, and can be determined as described herein. The phrase "normalizing gene expression in a diseased cell" refers to an action to normalize the expression of a substantial number of genes in the diseased cell.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term

should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

The phrase "nucleic acid corresponding to a gene" refers to a nucleic acid that can be used for detecting the gene, e.g., a nucleic acid which is capable of hybridizing specifically to the gene.

The term "percent identical" refers to sequence identity between two amino acid sequences or between two nucleotide sequences. Identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology, similarity, or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including FASTA, BLAST, or ENTREZ. FASTA and BLAST are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with, e.g., default settings. ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Md. In one embodiment, the percent identity of two sequences can be determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences. Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. *See* Meth. Mol. Biol. 70: 173-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman

algorithm to score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases. Databases with individual sequences are described in Methods in Enzymology, ed. Doolittle, *supra*. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

"Perfectly matched" in reference to a duplex means that the poly- or oligonucleotide strands making up the duplex form a double stranded structure with one other such that every nucleotide in each strand undergoes Watson-Crick basepairing with a nucleotide in the other strand. The term also comprehends the pairing of nucleoside analogs, such as deoxyinosine, nucleosides with 2-aminopurine bases, and the like, that may be employed. A mismatch in a duplex between a target polynucleotide and an oligonucleotide or olynucleotide means that a pair of nucleotides in the duplex fails to undergo Watson-Crick bonding. In reference to a triplex, the term means that the triplex consists of a perfectly matched duplex and a third strand in which every nucleotide undergoes Hoogsteen or reverse Hoogsteen association with a basepair of the perfectly matched duplex.

A "plurality" refers to two or more.

As used herein, a nucleic acid or other molecule attached to an array, is referred to as a "probe" or "capture probe." When an array contains several probes corresponding to one gene, these probes are referred to as "gene-probe set." A gene-probe set can consist of, e.g., 2 to 10 probes, preferably from 2 to 5 probes and most preferably about 5 probes.

A "significant similarity" between the level of expression of a gene in two cells or tissues generally refers to a difference in expression levels of a factor of at most about 10% (i.e., 1.1 fold), 25% (i.e., 1.25 fold), 50% (i.e., 1.5 fold), 75% (i.e., 1.75 fold), 90% (i.e., 1.9 fold), 2 fold, 2.5 fold, 3 fold, 5 fold, or 10 fold. Expression levels can be raw data or they can averaged or normalized data, e.g., normalized relative to normal controls. A "significant difference" between the level of expression of a gene in two cells or tissues generally refers to a difference in expression levels of a factor of at least about 10% (i.e., 1.1 fold), 25% (i.e., 1.25 fold), 50% (i.e., 1.5 fold), 75% (i.e., 1.75 fold), 90% (i.e., 1.9 fold), 2 fold, 2.5 fold, 3 fold, 5 fold, 10 fold, 50 fold or 100 fold. Whether the expression of a particular gene in two samples is significantly different or similar also depends on the gene itself and, e.g., its variability in expression between different individuals. It is within

the skill in the art to determine whether expression levels are significantly similar or different.

An expression profile in one cell or tissue is "significantly similar" to an expression profile in another cell or tissue when the level of expression of the genes in the two expression profiles are sufficiently similar that the similarity is indicative of a common characteristic, e.g., being of the same cell type, or being characteristic of a disease. "Similarity" between an expression profile of a cell or tissue, e.g., of a subject, and a set of data representing an expression profile characteristic of a disease can be based on the presence or absence in the cell or tissue of certain RNAs and/or certain levels of certain RNAs of genes having a high probability of being associated with the disease. A high probability of being associated with a disease can be, e.g., the presence of RNA or of certain levels of RNA of particular genes which are over-expressed or under-expressed, in at least about 50%, 60%, 70%, 80%, 90%, or 100% of patients having the disease. A similarity with an expression profile of a patient can be based on higher or lower expression levels of a factor of at most about 10%, 25%, 50%, 75%, 1.5 fold, 2 fold, 2.5 fold, 3 fold, 5 fold or 10 fold of at least about 50%, 60%, 70%, 80%, 90%, or 100% of genes, or at least about 10, 50, 100, 200, 300 genes, that are up- or down-regulated in at least about 50%, 60%, 70%, 80%, 90%, or 100% of patients.

"Small molecule" as used herein, is meant to refer to a composition, which has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon-containing) or inorganic molecules. Many pharmaceutical companies have extensive libraries of chemical and/or biological mixtures, often fungal, bacterial, or algal extracts, which can be screened with any of the assays of the invention to identify compounds that modulate a bioactivity.

The term "specific hybridization" of a probe to a target site of a template nucleic acid refers to hybridization of the probe predominantly to the target, such that the hybridization signal can be clearly interpreted. As further described herein, such conditions resulting in specific hybridization vary depending on the length of the region of homology, the GC content of the region, the melting temperature "Tm" of the hybrid. Hybridization conditions will thus vary in the salt content, acidity, and temperature of the hybridization solution and the washes.

A "subject" can be a mammal, e.g., a human, primate, ovine, bovine, porcine, equine, feline, canine and a rodent (rat or mouse).

The term "treating" a disease in a subject or "treating" a subject having a disease refers to providing the subject with a pharmaceutical treatment, e.g., the administration of a drug, such that at least one symptom of the disease is decreased. Treating a disease can be preventing the disease, improving the disease or curing the disease.

The phrase "value representing the level of expression of a gene" refers to a raw number which reflects the mRNA or polypeptide level of a particular gene in a cell or biological sample, e.g., obtained from analytical tools for measuring RNA or polypeptide levels.

A "variant" of a polypeptide refers to a polypeptide having the amino acid sequence of the polypeptide, in which one or more amino acid residues are altered. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "non-conservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR). The term "variant," when used in the context of a polynucleotide sequence, encompasses a polynucleotide sequence related to that of a gene of interest or the coding sequence thereof. This definition may also include, for example, "allelic," "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

2. Diagnostic and prognostic methods and compositions

The invention provides gene expression profiles over time during bone formation, e.g., endochondral bone formation induced by BMP-2. Since these expression profiles are characteristic of bone and cartilage formation, measuring the level of expression or level of product of one or more genes identified in these expression profiles, e.g., genes set forth in Tables 1, 2, 5 and/or 6, during bone or cartilage formation is expected to reveal any abnormalities in these processes. Abnormalities can then be treated appropriately, such as described below.

Exemplary situations in which one may wish to monitor bone or cartilage formation or resorption include diseases relating to bone or cartilage formation or bone or cartilage resorption, such as osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; periondontal disease; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss cause by an inflammatory disease, e.g., rheumatoid arthritis and osteoarthritis; wound healing and related tissue repair (e.g., burns, incisions and ulcers) and bone fractures. Bone or cartilage formation or resoption can also be monitored during treatment of any of the above-mentioned diseases and any conditions in which bone or cartilage formation is induced, such as by therapeutics, e.g., bone morphogenetic proteins. Situations in which bone or cartilage formation may be induced include healing of fractures, e.g., in closed and open fracture reduction; improved fixation of artificial joints; repair of congenital, trauma induced, or oncologic resection induced craniofacial defects; tooth repair processes and plastic, e.g., cosmetic plastic, surgery.

Accordingly, the invention provides methods for diagnosing and monitoring the development of any disease relating to bone or cartilage formation or resorption, such as the diseases set forth above. The methods of the invention also allow to distinguish one disease from another, where such distinction is not possible based on phenotypic or histologic examination.

In yet another embodiment, the methods of the invention allow to determine the stage of a particular disease. For example, by knowing the level of expression of certain genes, the state of bone or cartilage development can be established.

The methods of the invention can also be used to monitor the treatment of a disease. Monitoring will reveal whether a subject is responsive to a treatment or whether the treatment should be modified.

Measuring the level of expression or the level of product of one or more genes described herein can also be used in prognostics, such as to determine whether a subject is likely to develop a disease relating to bone or cartilage formation or resorption. For example a subject whose family is associated with such disorders can be monitored to determine whether he or she will develop such a disorder.

Another situation during which gene expression can be monitored is during in vitro bone or cartilage formation, e.g., induced by a bone morphogenetic protein. *In vitro* synthesized bone or cartilage can be used for implanting into subject in need thereof, such as subjects having suffered bone loss, e.g., resulting from cancer or osteoporosis.

In one embodiment, a sample is obtained from a subject, e.g., a human subject, and the level of expression of one or more genes, such as genes listed in any of Tables 1, 2, 5 and/or 6, is determined. The particular method used for obtaining a sample will depend on the site of the sample to be obtained. Samples can be obtained according to methods known in the art. As few as one cell may be sufficient for determining gene expression. In other embodiments, the presence of proteins is determined in a bodily fluid, e.g., blood or synovial fluid. Gene expression can be determined according to methods known in the art, such as reverse transcriptase polymerase chain reaction (RT-PCR); nucleic acid arrays; dotblots; and in situ hybridization, as further described herein. In other embodiments, the level of protein is measured, such as by immunohistochemistry, ELISA, or immunoprecipitation.

In certain embodiments, several samples are obtained consecutively, and a change of expression is monitored over time. For example, samples may be obtained about every 1, 2, 3, 5, 6, 12, 24, 36 or 48 hours.

The level of expression of one or more genes in a sample can be compared to the level of expression of these genes in a control sample. A control sample may be obtained, e.g., from the same patient, but at a different site, or from a healthy subject. Alternatively, the level of expression of the genes in the sample is compared to values stored in a data-readable medium, such as the values set forth in Tables 1, 2, 5 and/or 6 or in Figures 1 or 2. The comparison can be conducted visually, or via a computer.

The presence of a bone or cartilage related disease or a defect in the treatment of such a disease may be indicated by differences in the level of expression of one or more genes in a sample and in the control sample. The differences in gene expression may be a difference of a factor of at least about 50%; 2; 3; 5; 10; 20; 50; or 100 fold. In other embodiments, an abnormality is revealed by comparing the level of expression of one or more genes over time with their expression in a control or healthy subject.

The diagnostic and prognostic assays may indicate a defect in cartilage or bone formation or the existence of inefficient treatment of a disease or healing, e.g., bone fracture healing. The assays may thus be followed by a proper treatment or correction of treatment. Exemplary treatments are provided below. Generally, any therapeutic known to correct the diagnosed abnormality can be used. For example, defective bone or cartilage formation may be corrected by administration of a bone morphogenetic protein (BMP), e.g., BPM-2 or BMP-4.

2.1. Use of arrays for determining the level of expression of genes

Generally, determining expression profiles with arrays involves the following steps: (a) obtaining a mRNA sample from a subject and preparing labeled nucleic acids therefrom (the "target nucleic acids" or "targets"); (b) contacting the target nucleic acids with the array under conditions sufficient for target nucleic acids to bind with corresponding probes on the array, e.g. by hybridization or specific binding; (c) optionally removing unbound targets from the array; (d) detecting bound targets, and (e) analyzing the results. As used herein, "nucleic acid probes" or "probes" are nucleic acids attached to the array, whereas "target nucleic acids" are nucleic acids that are hybridized to the array. Each of these steps is described in more detail below.

(i) Obtaining a mRNA sample of a subject

In one embodiment, one or more cells from the subject to be tested are obtained and RNA is isolated from the cells. In a preferred embodiment, a sample of bone, cartilage, mesenchymal cells, synovial fluid, synovium, tumor or other tissue likely to be affected by the disorder to be diagnosed or monitored, are obtained from the subject according to methods known in the art. Cells from which expression levels may be obtained include macrophages, fibroblasts, chondrocyte-like cells, chondrocytes, chondroblasts, bone marrow cells, osteoblast, osteocytes, osteoclasts, and osteogenic precursor cells, e.g., mesenchymal cells. When obtaining the cells, it is preferable to obtain a sample containing

predominantly cells of the desired type, e.g., a sample of cells in which at least about 50%, preferably at least about 60%, even more preferably at least about 70%, 80% and even more preferably, at least about 90% of the cells are of the desired type. A higher percentage of cells of the desired type is preferable, since such a sample is more likely to provide clear gene expression data.

It is also possible to obtain a cell sample from a subject, and then to enrich it for a desired cell type. Cells can also be isolated from other cells using a variety of techniques, such as isolation with an antibody binding to an epitope on the cell surface of the desired cell type. Another method that can be used includes negative selection using antibodies to cell surface markers to selectively enrich for a specific cell type without activating the cell by receptor engagement. Where the desired cells are in a solid tissue, particular cells can be dissected out, e.g., by microdissection. Exemplary cells that one may want to enrich for include mesenchymal cells, such as muscular mesenchymal cells, osteoblasts, osteocytes, chondroblasts, chondrocytes, tumor cells and other bone or cartilage cells.

In one embodiment, RNA is obtained from a single cell. For example, a cell can be isolated from a tissue sample by laser capture microdissection (LCM). Using this technique, a cell can be isolated from a tissue section, including a stained tissue section, thereby assuring that the desired cell is isolated (*see, e.g.*, Bonner et al. (1997) Science 278: 1481; Emmert-Buck et al. (1996) Science 274:998; Fend et al. (1999) Am. J. Path. 154: 61 and Murakami et al. (2000) Kidney Int. 58:1346). For example, Murakami et al., *supra*, describe isolation of a cell from a previously immunostained tissue section.

It is also be possible to obtain cells from a subject and culture the cells *in vitro*, such as to obtain a larger population of cells from which RNA can be extracted. Methods for establishing cultures of non-transformed cells, i.e., primary cell cultures, are known in the art.

When isolating RNA from tissue samples or cells from individuals, it may be important to prevent any further changes in gene expression after the tissue or cells has been removed from the subject. Changes in expression levels are known to change rapidly following perturbations, e.g., heat shock or activation with lipopolysaccharide (LPS) or other reagents. In addition, the RNA in the tissue and cells may quickly become degraded. Accordingly, in a preferred embodiment, the tissue or cells obtained from a subject is snap frozen as soon as possible.

RNA can be extracted from the tissue sample by a variety of methods, e.g., those described in the Examples or guanidium thiocyanate lysis followed by CsCl centrifugation (Chirgwin et al., 1979, Biochemistry 18:5294-5299). RNA from single cells can be obtained as described in methods for preparing cDNA libraries from single cells, such as those described in Dulac, C. (1998) Curr. Top. Dev. Biol. 36, 245 and Jena et al. (1996) J. Immunol. Methods 190:199. Care to avoid RNA degradation must be taken, e.g., by inclusion of RNAsin.

The RNA sample can then be enriched in particular species. In one embodiment, poly(A)+ RNA is isolated from the RNA sample. In general, such purification takes advantage of the poly-A tails on mRNA. In particular and as noted above, poly-T oligonucleotides may be immobilized on a solid support to serve as affinity ligands for mRNA. Kits for this purpose are commercially available, e.g., the MessageMaker kit (Life Technologies, Grand Island, NY).

In a preferred embodiment, the RNA population is enriched in sequences of interest, such as those of genes listed in Tables 1, 2, 5 and/or 6. Enrichment can be undertaken, e.g., by primer-specific cDNA synthesis, or multiple rounds of linear amplification based on cDNA synthesis and template-directed *in vitro* transcription (*see, e.g.*, Wang et al. (1989) PNAS 86, 9717; Dulac et al., *supra*, and Jena et al., *supra*).

The population of RNA, enriched or not in particular species or sequences, can further be amplified. Such amplification is particularly important when using RNA from a single or a few cells. A variety of amplification methods are suitable for use in the methods of the invention, including, e.g., PCR; ligase chain reaction (LCR) (*See, e.g.*, Wu and Wallace, Genomics 4, 560 (1989), Landegren et al., Science 241, 1077 (1988)); self-sustained sequence replication (SSR) (*see, e.g.*, Guatelli et al., Proc. Nat. Acad. Sci. USA, 87, 1874 (1990)); nucleic acid based sequence amplification (NASBA) and transcription amplification (*see, e.g.*, Kwoh et al., Proc. Natl. Acad. Sci. USA 86, 1173 (1989)). For PCR technology, *see, e.g.*, PCR Technology: Principles and Applications for DNA Amplification (ed. H. A. Erlich, Freeman Press, N.Y., N.Y., 1992); PCR Protocols: A Guide to Methods and applications (eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. No. 4,683,202. Methods of amplification are described, e.g., in Ohyama et al. (2000) BioTechniques 29:530; Luo et al. (1999) Nat. Med. 5, 117; Hegde et al. (2000)

BioTechniques 29:548; Kacharmina et al. (1999) Meth. Enzymol. 303:3; Livesey et al. (2000) Curr. Biol. 10:301; Spirin et al. (1999) Invest. Ophtalmol. Vis. Sci. 40:3108; and Sakai et al. (2000) Anal. Biochem. 287:32. RNA amplification and cDNA synthesis can also be conducted in cells *in situ* (*see, e.g.*, Eberwine et al. (1992) PNAS 89:3010).

One of skill in the art will appreciate that whatever amplification method is used, if a quantitative result is desired, care must be taken to use a method that maintains or controls for the relative frequencies of the amplified nucleic acids to achieve quantitative amplification. Methods of "quantitative" amplification are well known to those of skill in the art. For example, quantitative PCR involves simultaneously co-amplifying a known quantity of a control sequence using the same primers. This provides an internal standard that may be used to calibrate the PCR reaction. A high density array may then include probes specific to the internal standard for quantification of the amplified nucleic acid.

One preferred internal standard is a synthetic AW106 cRNA. The AW106 ERNA is combined with RNA isolated from the sample according to standard techniques known to those of skilled in the art. The RNA is then reverse transcribed using a reverse transcriptase to provide copy DNA. The cDNA sequences are then amplified (e.g., by PCR) using labeled primers. The amplification products are separated, typically by electrophoresis, and the amount of radioactivity (proportional to the amount of amplified product) is determined. The amount of mRNA in the sample is then calculated by comparison with the signal produced by the known AW106 RNA standard. Detailed protocols for quantitative PCR are provided in PCR Protocols, A Guide to Methods and Applications, Innis et al., Academic Press, Inc. N.Y., (1990).

In a preferred embodiment, a sample mRNA is reverse transcribed with a reverse transcriptase and a primer consisting of oligo(dT) and a sequence encoding the phage T7 promoter to provide single stranded DNA template. The second DNA strand is polymerized using a DNA polymerase. After synthesis of double-stranded cDNA, T7 RNA polymerase is added and RNA is transcribed from the cDNA template. Successive rounds of transcription from each single cDNA template results in amplified RNA. Methods of *in vitro* polymerization are well known to those of skill in the art (See, e.g., Sambrook, (*supra*) and this particular method is described in detail by Van Gelder, et al., Proc. Natl. Acad. Sci. USA, 87: 1663-1667 (1990) who demonstrate that *in vitro* amplification according to this method preserves the relative frequencies of the various RNA transcripts). Moreover, Eberwine et al. Proc. Natl. Acad. Sci. USA, 89: 3010-3014 provide a protocol that uses two

rounds of amplification via *in vitro* transcription to achieve greater than 10^6 fold amplification of the original starting material, thereby permitting expression monitoring even where biological samples are limited.

It will be appreciated by one of skill in the art that the direct transcription method described above provides an antisense (aRNA) pool. Where antisense RNA is used as the target nucleic acid, the oligonucleotide probes provided in the array are chosen to be complementary to subsequences of the antisense nucleic acids. Conversely, where the target nucleic acid pool is a pool of sense nucleic acids, the oligonucleotide probes are selected to be complementary to subsequences of the sense nucleic acids. Finally, where the nucleic acid pool is double stranded, the probes may be of either sense as the target nucleic acids include both sense and antisense strands.

(ii) Labeling of the nucleic acids to be analyzed

Generally, the target molecules will be labeled to permit detection of hybridization of target molecules to a microarray. By "labeled" is meant that the probe comprises a member of a signal producing system and is thus detectable, either directly or through combined action with one or more additional members of a signal producing system. Examples of directly detectable labels include isotopic and fluorescent moieties incorporated into, usually covalently bonded to, a moiety of the probe, such as a nucleotide monomeric unit, e.g. dNMP of the primer, or a photoactive or chemically active derivative of a detectable label which can be bound to a functional moiety of the probe molecule.

Nucleic acids can be labeled after or during enrichment and/or amplification of RNAs. For example, labeled cDNA can be prepared from mRNA by oligo dT-primed or random-primed reverse transcription, both of which are well known in the art (*see, e.g.*, Klug and Berger, 1987, Methods Enzymol. 152:316-325). Reverse transcription may be carried out in the presence of a dNTP conjugated to a detectable label, most preferably a fluorescently labeled dNTP. Alternatively, isolated mRNA can be converted to labeled antisense RNA synthesized by *in vitro* transcription of double-stranded cDNA in the presence of labeled dNTPs (Lockhart et al., 1996, Expression monitoring by hybridization to high-density oligonucleotide arrays, Nature Biotech. 14:1675). In alternative embodiments, the cDNA or RNA probe can be synthesized in the absence of detectable label and may be labeled subsequently, e.g., by incorporating biotinylated dNTPs or rNTP, or some similar means (e.g., photo-cross-linking a psoralen derivative of biotin to RNAs),

followed by addition of labeled streptavidin (e.g., phycoerythrin-conjugated streptavidin) or the equivalent.

In one embodiment, labeled cDNA is synthesized by incubating a mixture containing RNA and 0.5 mM dGTP, dATP and dCTP plus 0.1 mM dTTP plus fluorescent deoxyribonucleotides (e.g., 0.1 mM Rhodamine 110 UTP (Perken Elmer Cetus) or 0.1 mM Cy3 dUTP (Amersham)) with reverse transcriptase (e.g., SuperScript.™.II, LTI Inc.) at 42 °C for 60 min.

Fluorescent moieties or labels of interest include coumarin and its derivatives, e.g. 7-amino-4-methylcoumarin, aminocoumarin, bodipy dyes, such as Bodipy FL, cascade blue, fluorescein and its derivatives, e.g. fluorescein isothiocyanate, Oregon green, rhodamine dyes, e.g. Texas red, tetramethylrhodamine, eosins and erythrosins, cyanine dyes, e.g. Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, FluorX, macrocyclic chelates of lanthanide ions, e.g. quantum dye™, fluorescent energy transfer dyes, such as thiazole orange-ethidium heterodimer, TOTAB, dansyl, etc. Individual fluorescent compounds which have functionalities for linking to an element desirably detected in an apparatus or assay of the invention, or which can be modified to incorporate such functionalities include, e.g., dansyl chloride; fluoresceins such as 3,6-dihydroxy-9-phenylxanthydrol; rhodamineisothiocyanate; N-phenyl 1-amino-8-sulfonatonaphthalene; N-phenyl 2-amino-6-sulfonatonaphthalene; 4-acetamido-4-isothiocyanato-stilbene-2,2'-disulfonic acid; pyrene-3-sulfonic acid; 2-toluidinonaphthalene-6-sulfonate; N-phenyl-N-methyl-2-aminoaphthalene-6-sulfonate; ethidium bromide; stebrine; auromine-0,2-(9'-anthroyl)palmitate; dansyl phosphatidylethanolamine; N,N'-dioctadecyl oxacarbocyanine: N,N'-dihexyl oxacarbocyanine; merocyanine, 4-(3'-pyrenyl)stearate; d-3-aminodesoxy-equilenin; 12-(9'-anthroyl)stearate; 2-methylanthracene; 9-vinylanthracene; 2,2'(vinylene-p-phenylene)bisbenzoxazole; p-bis(2- -methyl-5-phenyl-oxazolyl))benzene; 6-dimethylamino-1,2-benzophenazin; retinol; bis(3'-aminopyridinium) 1,10-decandiyl diiodide; sulfonaphthylhydrazone of hellibrienin; chlorotetracycline; N-(7-dimethylamino-4-methyl-2-oxo-3-chromenyl)maleimide; N-(p-(2benzimidazolyl)-phenyl)maleimide; N-(4-fluoranthyl)maleimide; bis(homovanillic acid); resazarin; 4-chloro-7-nitro-2,1,3-benzooxadiazole; merocyanine 540; resorufin; rose bengal; and 2,4-diphenyl-3(2H)-furanone. (*see, e.g.*, Kricka, 1992, Nonisotopic DNA Probe Techniques, Academic Press San Diego, Calif.). Many fluorescent tags are commercially available from SIGMA chemical company (Saint Louis, Mo.), Amersham, Molecular Probes, R&D systems

(Minneapolis, Minn.), Pharmacia LKB Biotechnology (Piscataway, N.J.), CLONTECH Laboratories, Inc. (Palo Alto, Calif.), Chem Genes Corp., Aldrich Chemical Company (Milwaukee, Wis.), Glen Research, Inc., GIBCO BRL Life Technologies, Inc. (Gaithersberg, Md.), Fluka Chemica-Biochemika Analytika (Fluka Chemie AG, Buchs, Switzerland), and Applied Biosystems (Foster City, Calif.) as well as other commercial sources known to one of skill.

Chemiluminescent labels include luciferin and 2,3-dihydrophthalazinediones, e.g., luminol.

Isotopic moieties or labels of interest include ^{32}P, ^{33}P, ^{35}S, ^{125}I, ^{2}H, ^{14}C, and the like (*see* Zhao et al., 1995, High density cDNA filter analysis: a novel approach for large-scale, quantitative analysis of gene expression, Gene 156:207; Pietu et al., 1996, Novel gene transcripts preferentially expressed in human muscles revealed by quantitative hybridization of a high density cDNA array, Genome Res. 6:492).

Labels may also be members of a signal producing system that act in concert with one or more additional members of the same system to provide a detectable signal. Illustrative of such labels are members of a specific binding pair, such as ligands, e.g. biotin, fluorescein, digoxigenin, antigen, polyvalent cations, chelator groups and the like, where the members specifically bind to additional members of the signal producing system, where the additional members provide a detectable signal either directly or indirectly, e.g. antibody conjugated to a fluorescent moiety or an enzymatic moiety capable of converting a substrate to a chromogenic product, e.g. alkaline phosphatase conjugate antibody and the like.

Additional labels of interest include those that provide for signal only when the probe with which they are associated is specifically bound to a target molecule, where such labels include: "molecular beacons" as described in Tyagi & Kramer, Nature Biotechnology (1996) 14:303 and EP 0 070 685 B1. Other labels of interest include those described in U.S. Pat. No. 5,563,037; WO 97/17471 and WO 97/17076.

In some cases, hybridized target nucleic acids may be labeled following hybridization. For example, where biotin labeled dNTPs are used in, e.g., amplification or transcription, streptavidin linked reporter groups may be used to label hybridized complexes.

In other embodiments, the target nucleic acid is not labeled. In this case, hybridization can be determined, e.g., by plasmon resonance, as described, e.g., in Thiel et al. (1997) Anal. Chem. 69:4948.

In one embodiment, a plurality (e.g., 2, 3, 4, 5 or more) of sets of target nucleic acids are labeled and used in one hybridization reaction ("multiplex" analysis). For example, one set of nucleic acids may correspond to RNA from one cell or tissue sample and another set of nucleic acids may correspond to RNA from another cell or tissue sample. The plurality of sets of nucleic acids can be labeled with different labels, e.g., different fluorescent labels which have distinct emission spectra so that they can be distinguished. The sets can then be mixed and hybridized simultaneously to one microarray.

For example, the two different cells can be a cell of a subject suspected of having a disease related to bone or cartilage formation or resoprtion and a counterpart normal cell. In another embodiment, e.g., for identifying drugs modulating bone formation, one biological sample contains cells that were exposed to a drug and the other biological sample contains cells that were not exposed to the drug. The cDNA derived from each of the two cell types are differently labeled so that they can be distinguished. In one embodiment, for example, cDNA from one sample is synthesized using a fluorescein-labeled dNTP, and cDNA from the second sample is synthesized using a rhodamine-labeled dNTP. When the two cDNAs are mixed and hybridized to the microarray, the relative intensity of signal from each cDNA set is determined for each site on the array, and any relative difference in abundance of a particular mRNA detected.

In the example described above, the cDNA from one sample will fluoresce green when the fluorophore is stimulated and the cDNA from the second sample will fluoresce red. As a result, if the two cells are essentially the same, the particular mRNA will be equally prevalent in both cells and, upon reverse transcription, red-labeled and green-labeled cDNA will be equally prevalent. When hybridized to the microarray, the binding site(s) for that species of RNA will emit wavelengths characteristic of both fluorophores (and appear brown in combination). In contrast, if the two cells are different, the ratio of green to red fluorescence will be different.

The use of a two-color fluorescence labeling and detection scheme to define alterations in gene expression has been described, e.g., in Shena et al., 1995, Quantitative monitoring of gene expression patterns with a complementary DNA microarray, Science 270:467-470. An advantage of using cDNA labeled with two different fluorophores is that

a direct and internally controlled comparison of the mRNA levels corresponding to each arrayed gene in two cell states can be made, and variations due to minor differences in experimental conditions (e.g, hybridization conditions) will not affect subsequent analyses.

Examples of distinguishable labels for use when hybridizing a plurality of target nucleic acids to one array are well known in the art and include: two or more different emission wavelength fluorescent dyes, like Cy3 and Cy5, combination of fluorescent proteins and dyes, like phicoerythrin and Cy5, two or more isotopes with different energy of emission, like ^{32}P and ^{33}P, gold or silver particles with different scattering spectra, labels which generate signals under different treatment conditions, like temperature, pH, treatment by additional chemical agents, etc., or generate signals at different time points after treatment. Using one or more enzymes for signal generation allows for the use of an even greater variety of distinguishable labels, based on different substrate specificity of enzymes (alkaline phosphatase/peroxidase).

Further, it is preferable in order to reduce experimental error to reverse the fluorescent labels in two-color differential hybridization experiments to reduce biases peculiar to individual genes or array spot locations. In other words, it is preferable to first measure gene expression with one labeling (e.g., labeling nucleic acid froma first cell with a first fluorochrome and nucleic acid from a second cell with a second fluorochrome) of the mRNA from the two cells being measured, and then to measure gene expression from the two cells with reversed labeling (e.g., labeling nucleic acid from the first cell with the second fluorochrome and nucleic acid from the second cell with the first fluorochrome). Multiple measurements over exposure levels and perturbation control parameter levels provide additional experimental error control.

The quality of labeled nucleic acids can be evaluated prior to hybridization to an array. For example, a sample of the labeled nucleic acids can be hybridized to probes derived from the 5', middle and 3' portions of genes known to be or suspected to be present in the nucleic acid sample. This will be indicative as to whether the labeled nucleic acids are full length nucleic acids or whether they are degraded. In one embodiment, the GeneChip® Test3 Array from Affymetrix (Santa Clara, CA) can be used for that purpose. This array contains probes representing a subset of characterized genes from several organisms including mammals. Thus, the quality of a labeled nucleic acid sample can be determined by hybridization of a fraction of the sample to an array, such as the GeneChip® Test3 Array from Affymetrix (Santa Clara, CA).

(iii) *Exemplary arrays*

Preferred arrays, e.g., microarrays, for use according to the invention include one or more probes of genes which are up- or down-regulated during bone or cartilage formation, such as one or more genes listed in any of Tables 1, 2, 5 and/or 6. The array may comprise probes corresponding to at least 10, preferably at least 20, at least 50, at least 100 or at least 1000 genes. The array may comprise probes corresponding to about 10%, 20%, 50%, 70%, 90% or 95% of the genes listed in any of Tables 1, 2, 5 and/or 6. The array may comprise probes corresponding to about 10%, 20%, 50%, 70%, 90% or 95% of the genes listed in any of Tables 1, 2, 5 and/or 6 whose expression increases or decreases at least about 2 fold, preferably at least about 3 fold, more preferably at least about 4 fold, 5 fold, 7 fold and most preferably at least about 10 fold during bone or cartilage formation. One array that can be used is the array used and described in the Examples.

There can be one or more than one probe corresponding to each gene on a microarray. For example, a microarray may contain from 2 to 20 probes corresponding to one gene and preferably about 5 to 10. The probes may correspond to the full length RNA sequence or complement thereof of genes that are up- or down-regulated during bone or cartilage formation, or they may correspond to a portion thereof, which portion is of sufficient length for permitting specific hybridization. Such probes may comprise from about 50 nucleotides to about 100, 200, 500, or 1000 nucleotides or more than 1000 nucleotides. As further described herein, microarrays may contain oligonucleotide probes, consisting of about 10 to 50 nucleotides, preferably about 15 to 30 nucleotides and even more preferably 20-25 nucleotides. The probes are preferably single stranded. The probe will have sufficient complementarity to its target to provide for the desired level of sequence specific hybridization (*see* below).

Typically, the arrays used in the present invention will have a site density of greater than 100 different probes per cm^2. Preferably, the arrays will have a site density of greater than 500/cm^2, more preferably greater than about 1000/cm^2, and most preferably, greater than about 10,000/cm^2. Preferably, the arrays will have more than 100 different probes on a single substrate, more preferably greater than about 1000 different probes still more preferably, greater than about 10,000 different probes and most preferably, greater than 100,000 different probes on a single substrate.

Microarrays can be prepared by methods known in the art, as described below, or they can be custom made by companies, e.g., Affymetrix (Santa Clara, CA).

Generally, two types of microarrays can be used. These two types are referred to as "synthesis" and "delivery." In the synthesis type, a microarray is prepared in a step-wise fashion by the in situ synthesis of nucleic acids from nucleotides. With each round of synthesis, nucleotides are added to growing chains until the desired length is achieved. In the delivery type of microarray, preprepared nucleic acids are deposited onto known locations using a variety of delivery technologies. Numerous articles describe the different microarray technologies, e.g., Shena et al. (1998) Tibtech 16: 301; Duggan et al. (1999) Nat. Genet. 21:10; Bowtell et al. (1999) Nat. Genet. 21: 25.

One novel synthesis technology is that developed by Affymetrix (Santa Clara, CA), which combines photolithography technology with DNA synthetic chemistry to enable high density oligonucleotide microarray manufacture. Such chips contain up to 400,000 groups of oligonucleotides in an area of about 1.6 cm^2. Oligonucleotides are anchored at the 3' end thereby maximizing the availability of single-stranded nucleic acid for hybridization. Generally such chips, referred to as "GeneChips®" contain several oligonucleotides of a particular gene, e.g., between 15-20, such as 16 oligonucleotides. Since Affymetrix (Santa Clara, CA) sells custom made microarrays, microarrays containing genes which are up- or down-regulated during bone formation can be ordered for purchase from Affymetrix (Santa Clara, CA).

Microarrays can also be prepared by mechanical microspotting, e.g., those commercialized at Synteni (Fremont, CA). According to these methods, small quantities of nucleic acids are printed onto solid surfaces. Microspotted arrays prepared at Synteni contain as many as 10,000 groups of cDNA in an area of about 3.6 cm^2.

A third group of microarray technologies consist in the "drop-on-demand" delivery approaches, the most advanced of which are the ink-jetting technologies, which utilize piezoelectric and other forms of propulsion to transfer nucleic acids from miniature nozzles to solid surfaces. Inkjet technologies is developed at several centers including Incyte Pharmaceuticals (Palo Alto, CA) and Protogene (Palo Alto, CA). This technology results in a density of 10,000 spots per cm^2. *See* also, Hughes et al. (2001) Nat. Biotechn. 19:342.

Arrays preferably include control and reference nucleic acids. Control nucleic acids are nucleic acids which serve to indicate that the hybridization was effective. For example, all Affymetrix (Santa Clara, CA) expression arrays contain sets of probes for several prokaryotic genes, e.g., bioB, bioC and bioD from biotin synthesis of *E. coli* and cre from P1 bacteriophage. Hybridization to these arrays is conducted in the presence of a mixture

of these genes or portions thereof, such as the mix provided by Affymetrix (Santa Clara, CA) to that effect (Part Number 900299), to thereby confirm that the hybridization was effective. Control nucleic acids included with the target nucleic acids can also be mRNA synthesized from cDNA clones by *in vitro* transcription. Other control genes that may be included in arrays are polyA controls, such as dap, lys, phe, thr, and trp (which are included on Affymetrix GeneChips®)

Reference nucleic acids allow the normalization of results from one experiment to another, and to compare multiple experiments on a quantitative level. Exemplary reference nucleic acids include housekeeping genes of known expression levels, e.g., GAPDH, hexokinase and actin.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases.

Arrays may also contain probes that hybridize to more than one allele of a gene. For example the array can contain one probe that recognizes allele 1 and another probe that recognizes allele 2 of a particular gene.

Microarrays can be prepared as follows. In one embodiment, an array of oligonucleotides is synthesized on a solid support. Exemplary solid supports include glass, plastics, polymers, metals, metalloids, ceramics, organics, etc. Using chip masking technologies and photoprotective chemistry it is possible to generate ordered arrays of nucleic acid probes. These arrays, which are known, e.g., as "DNA chips," or as very large scale immobilized polymer arrays ("VLSIPS™" arrays) can include millions of defined probe regions on a substrate having an area of about 1 cm^2 to several cm^2, thereby incorporating sets of from a few to millions of probes (*see, e.g.*, U.S. Patent No. 5,631,734).

The construction of solid phase nucleic acid arrays to detect target nucleic acids is well described in the literature. *See*, Fodor et al. (1991) Science, 251: 767-777; Sheldon et al. (1993) Clinical Chemistry 39(4): 718-719; Kozal et al. (1996) Nature Medicine 2(7): 753-759 and Hubbell U.S. Pat. No. 5,571,639; Pinkel et al. PCT/US95/16155 (WO 96/17958); U.S. Pat. Nos. 5,677,195; 5,624,711; 5,599,695; 5,451,683; 5,424,186; 5,412,087; 5,384,261; 5,252,743 and 5,143,854; PCT Patent Publication Nos. 92/10092 and 93/09668; and PCT WO 97/10365. In brief, a combinatorial strategy allows for the synthesis of arrays containing a large number of probes using a minimal number of

synthetic steps. For instance, it is possible to synthesize and attach all possible DNA 8 mer oligonucleotides (48, or 65,536 possible combinations) using only 32 chemical synthetic steps. In general, VLSIPS™ procedures provide a method of producing 4n different oligonucleotide probes on an array using only 4n synthetic steps (*see, e.g.*, U.S. Pat. No. 5,631,734 5; 143,854 and PCT Patent Publication Nos. WO 90/15070; WO 95/11995 and WO 92/10092).

Light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface can be performed with automated phosphoramidite chemistry and chip masking techniques similar to photoresist technologies in the computer chip industry. Typically, a glass surface is derivatized with a silane reagent containing a functional group, e.g., a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5'-photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface.

Algorithms for design of masks to reduce the number of synthesis cycles are described by Hubbel et al., U.S. Pat. No. 5,571,639 and U.S. Pat. No. 5,593,839. A computer system may be used to select nucleic acid probes on the substrate and design the layout of the array as described in U.S. Pat. No. 5,571,639.

Another method for synthesizing high density arrays is described in U.S. Patent No. 6,083,697. This method utilizes a novel chemical amplification process using a catalyst system which is initiated by radiation to assist in the synthesis the polymer sequences. Such methods include the use of photosensitive compounds which act as catalysts to chemically alter the synthesis intermediates in a manner to promote formation of polymer sequences. Such photosensitive compounds include what are generally referred to as radiation-activated catalysts (RACs), and more specifically photo activated catalysts (PACs). The RACs can by themselves chemically alter the synthesis intermediate or they can activate an autocatalytic compound which chemically alters the synthesis intermediate in a manner to allow the synthesis intermediate to chemically combine with a later added synthesis intermediate or other compound.

Arrays can also be synthesized in a combinatorial fashion by delivering monomers to cells of a support by mechanically constrained flowpaths. *See* Winkler et al., EP 624,059. Arrays can also be synthesized by spotting monomers reagents on to a support using an ink jet printer. *See* id. and Pease et al., EP 728,520.

cDNA probes can be prepared according to methods known in the art and further described herein, e.g., reverse-transcription PCR (RT-PCR) of RNA using sequence specific primers. Oligonucleotide probes can be synthesized chemically. Sequences of the genes or cDNA from which probes are made can be obtained, e.g., from GenBank, other public databases or publications.

Nucleic acid probes can be natural nucleic acids, chemically modified nucleic acids, e.g., composed of nucleotide analogs, as long as they have activated hydroxyl groups compatible with the linking chemistry. The protective groups can, themselves, be photolabile. Alternatively, the protective groups can be labile under certain chemical conditions, e.g., acid. In this example, the surface of the solid support can contain a composition that generates acids upon exposure to light. Thus, exposure of a region of the substrate to light generates acids in that region that remove the protective groups in the exposed region. Also, the synthesis method can use 3'- protected 5'-0-phosphoramidite-activated deoxynucleoside. In this case, the oligonucleotide is synthesized in the 5' to 3' direction, which results in a free 5' end.

Oligonucleotides of an array can be synthesized using a 96 well automated multiplex oligonucleotide synthesizer (A.M.O.S.) that is capable of making thousands of oligonucleotides (Lashkari et al. (1995) PNAS 93: 7912) can be used.

It will be appreciated that oligonucleotide design is influenced by the intended application. For example, it may be desirable to have similar melting temperatures for all of the probes. Accordingly, the length of the probes are adjusted so that the melting temperatures for all of the probes on the array are closely similar (it will be appreciated that different lengths for different probes may be needed to achieve a particular T[m] where different probes have different GC contents). Although melting temperature is a primary consideration in probe design, other factors are optionally used to further adjust probe construction, such as selecting against primer self-complementarity and the like.

Arrays, e.g., microarrrays, may conveniently be stored following fabrication or purchase for use at a later time. Under appropriate conditions, the subject arrays are capable of being stored for at least about 6 months and may be stored for up to one year or

longer. Arrays are generally stored at temperatures between about -20° C to room temperature, where the arrays are preferably sealed in a plastic container, e.g. bag, and shielded from light.

(iv) *Hybridization of the target nucleic acids to the microarray*

The next step is to contact the target nucleic acids with the array under conditions sufficient for binding between the target nucleic acids and the probes of the array. In a preferred embodiment, the target nucleic acids will be contacted with the array under conditions sufficient for hybridization to occur between the target nucleic acids and probes on the microarray, where the hybridization conditions will be selected in order to provide for the desired level of hybridization specificity.

Contact of the array and target nucleic acids involves contacting the array with an aqueous medium comprising the target nucleic acids. Contact may be achieved in a variety of different ways depending on specific configuration of the array. For example, where the array simply comprises the pattern of size separated probes on the surface of a "plate-like" rigid substrate, contact may be accomplished by simply placing the array in a container comprising the target nucleic acid solution, such as a polyethylene bag, and the like. In other embodiments where the array is entrapped in a separation media bounded by two rigid plates, the opportunity exists to deliver the target nucleic acids via electrophoretic means. Alternatively, where the array is incorporated into a biochip device having fluid entry and exit ports, the target nucleic acid solution can be introduced into the chamber in which the pattern of target molecules is presented through the entry port, where fluid introduction could be performed manually or with an automated device. In multiwell embodiments, the target nucleic acid solution will be introduced in the reaction chamber comprising the array, either manually, e.g. with a pipette, or with an automated fluid handling device.

Contact of the target nucleic acid solution and the probes will be maintained for a sufficient period of time for binding between the target and the probe to occur. Although dependent on the nature of the probe and target, contact will generally be maintained for a period of time ranging from about 10 min to 24 hrs, usually from about 30 min to 12 hrs and more usually from about 1 hr to 6 hrs.

When using commercially available microarrays, adequate hybridization conditions are provided by the manufacturer. When using non-commercial microarrays, adequate hybridization conditions can be determined based on the following hybridization

guidelines, as well as on the hybridization conditions described in the numerous published articles on the use of microarrays.

Nucleic acid hybridization and wash conditions are optimally chosen so that the probe "specifically binds" or "specifically hybridizes" to a specific array site, i.e., the probe hybridizes, duplexes or binds to a sequence array site with a complementary nucleic acid sequence but does not hybridize to a site with a non-complementary nucleic acid sequence. As used herein, one polynucleotide sequence is considered complementary to another when, if the shorter of the polynucleotides is less than or equal to 25 bases, there are no mismatches using standard base-pairing rules or, if the shorter of the polynucleotides is longer than 25 bases, there is no more than a 5% mismatch. Preferably, the polynucleotides are perfectly complementary (no mismatches). It can easily be demonstrated that specific hybridization conditions result in specific hybridization by carrying out a hybridization assay including negative controls.

Hybridization is carried out in conditions permitting essentially specific hybridization. The length of the probe and GC content will determine the Tm of the hybrid, and thus the hybridization conditions necessary for obtaining specific hybridization of the probe to the template nucleic acid. These factors are well known to a person of skill in the art, and can also be tested in assays. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993), "Laboratory Techniques in biochemistry and molecular biology-hybridization with nucleic acid probes." Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Highly stringent conditions are selected to be equal to the Tm point for a particular probe. Sometimes the term "Td" is used to define the temperature at which at least half of the probe dissociates from a perfectly matched target nucleic acid. In any case, a variety of estimation techniques for estimating the Tm or Td are available, and generally described in Tijssen, *supra*. Typically, G-C base pairs in a duplex are estimated to contribute about 3°C to the Tm, while A-T base pairs are estimated to contribute about 2°C, up to a theoretical maximum of about 80-100°C. However, more sophisticated models of Tm and Td are available and appropriate in which G-C stacking interactions, solvent effects, the desired assay temperature and the like are taken into account. For example,

probes can be designed to have a dissociation temperature (Td) of approximately 60°C, using the formula: Td = (((((3 x #GC) + (2 x #AT)) x 37) - 562)/#bp) - 5; where #GC, #AT, and #bp are the number of guanine-cytosine base pairs, the number of adenine-thymine base pairs, and the number of total base pairs, respectively, involved in the annealing of the probe to the template DNA.

The stability difference between a perfectly matched duplex and a mismatched duplex, particularly if the mismatch is only a single base, can be quite small, corresponding to a difference in Tm between the two of as little as 0.5 degrees. *See* Tibanyenda, N. et al., Eur. J. Biochem. 139:19 (1984) and Ebel, S. et al., Biochem. 31:12083 (1992). More importantly, it is understood that as the length of the homology region increases, the effect of a single base mismatch on overall duplex stability decreases.

Theory and practice of nucleic acid hybridization is described, e.g., in S. Agrawal (ed.) Methods in Molecular Biology, volume 20; and Tijssen (1993) Laboratory Techniques in biochemistry and molecular biology-hybridization with nucleic acid probes, e.g., part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays", Elsevier, New York provide a basic guide to nucleic acid hybridization.

Certain microarrays are of "active" nature, i.e., they provide independent electronic control over all aspects of the hybridization reaction (or any other affinity reaction) occurring at each specific microlocation. These devices provide a new mechanism for affecting hybridization reactions which is called electronic stringency control (ESC). Such active devices can electronically produce "different stringency conditions" at each microlocation. Thus, all hybridizations can be carried out optimally in the same bulk solution. These arrays are described in U.S. Patent No. 6,051,380 by Sosnowski et al.

In a preferred embodiment, background signal is reduced by the use of a detergent (e.g, C-TAB) or a blocking reagent (e.g., sperm DNA, cot-1 DNA, etc.) during the hybridization to reduce non-specific binding. In a particularly preferred (embodiment, the hybridization is performed in the presence of about 0.5 mg/ml DNA (e.g., herring sperm DNA). The use of blocking agents in hybridization is well known to those of skill in the art (see, e.g., Chapter 8 in Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24: Hybridization With Nucleic Acid Probes, P. Tijssen, ed. Elsevier, N.Y., (1993)).

The method may or may not further comprise a non-bound label removal step prior to the detection step, depending on the particular label employed on the target nucleic acid. For example, in certain assay formats (e.g., "homogenous assay formats") a detectable

signal is only generated upon specific binding of target to probe. As such, in these assay formats, the hybridization pattern may be detected without a non-bound label removal step. In other embodiments, the label employed will generate a signal whether or not the target is specifically bound to its probe. In such embodiments, the non-bound labeled target is removed from the support surface. One means of removing the non-bound labeled target is to perform the well known technique of washing, where a variety of wash solutions and protocols for their use in removing non-bound label are known to those of skill in the art and may be used. Alternatively, non-bound labeled target can be removed by electrophoretic means.

Where all of the target sequences are detected using the same label, different arrays will be employed for each physiological source or time point (where different could include using the same array at different times). The above methods can be varied to provide for multiplex analysis, by employing different and distinguishable labels for the different target populations (representing each of the different physiological sources or time points being assayed). According to this multiplex method, the same array is used at the same time for each of the different target populations.

In another embodiment, hybridization is monitored in real time using a charge-coupled device (CCD) imaging camera (Guschin et al. (1997) Anal. Biochem. 250:203). Synthesis of arrays on optical fibre bundles allows easy and sensitive reading (Healy et al. (1997) Anal. Biochem. 251:270). In another embodiment, real time hybridization detection is carried out on microarrays without washing using evanescent wave effect that excites only fluorophores that are bound to the surface (*see, e.g.*, Stimpson et al. (1995) PNAS 92:6379).

(v) Detection of hybridization and analysis of results

The above steps result in the production of hybridization patterns of target nucleic acid on the array surface. These patterns may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular label of the target nucleic acid. Representative detection means include scintillation counting, autoradiography, fluorescence measurement, colorimetric measurement, light emission measurement, light scattering, and the like.

One method of detection includes an array scanner that is commercially available from Affymetrix (Santa Clara, CA), e.g., the 417™ Arrayer, the 418™ Array Scanner, or the Agilent GeneArray™ Scanner. This scanner is controlled from the system computer

with a Windows^R interface and easy-to-use software tools. The output is a 16-bit.tif file that can be directly imported into or directly read by a variety of software applications. Preferred scanning devices are described in, e.g., U.S. Pat. Nos. 5,143,854 and 5,424,186.

When fluorescently labeled probes are used, the fluorescence emissions at each site of a transcript array can be detected by scanning confocal laser microscopy. In one embodiment, a separate scan, using the appropriate excitation line, is carried out for each of the two fluorophores used. Alternatively, a laser can be used that allows simultaneous specimen illumination at wavelengths specific to the two fluorophores and emissions from the two fluorophores can be analyzed simultaneously (*see* Shalon et al., 1996, A DNA microarray system for analyzing complex DNA samples using two-color fluorescent probe hybridization, Genome Research 6:639-645). In a preferred embodiment, the arrays are scanned with a laser fluorescent scanner with a computer controlled X-Y stage and a microscope objective. Sequential excitation of the two fluorophores can be achieved with a multi-line, mixed gas laser and the emitted light is split by wavelength and detected with two photomultiplier tubes. In one embodiment in which fluorescent target nucleic acids are used, the arrays may be scanned using lasers to excite fluorescently labeled targets that have hybridized to regions of probe arrays, which can then be imaged using charged coupled devices ("CCDs") for a wide field scanning of the array. Fluorescence laser scanning devices are described, e.g., in Schena et al., 1996, Genome Res. 6:639-645. Alternatively, the fiber-optic bundle described by Ferguson et al., 1996, Nature Biotech. 14:1681-1684, may be used to monitor mRNA abundance levels.

Following the data gathering operation, the data will typically be reported to a data analysis operation. To facilitate the sample analysis operation, the data obtained by the reader from the device will typically be analyzed using a digital computer. Typically, the computer will be appropriately programmed for receipt and storage of the data from the device, as well as for analysis and reporting of the data gathered, e.g., subtrackion of the background, deconvolution multi-color images, flagging or removing artifacts, verifying that controls have performed properly, normalizing the signals, interpreting fluorescence data to determine the amount of hybridized target, normalization of background and single base mismatch hybridizations, and the like. In a preferred embodiment, a system comprises a search function that allows one to search for specific patterns, e.g., patterns relating to differential gene expression of genes which are up- or down-regulated during

bone or cartilage formation. A system preferably allows one to search for patterns of gene expression between more than two samples.

A desirable system for analyzing data is a general and flexible system for the visualization, manipulation, and analysis of gene expression data. Such a system preferably includes a graphical user interface for browsing and navigating through the expression data, allowing a user to selectively view and highlight the genes of interest. The system also preferably includes sort and search functions and is preferably available for general users with PC, Mac or Unix workstations. Also preferably included in the system are clustering algorithms that are qualitatively more efficient than existing ones. The accuracy of such algorithms is preferably hierarchically adjustable so that the level of detail of clustering can be systematically refined as desired.

Various algorithms are available for analyzing the gene expression profile data, e.g., the type of comparisons to perform. In certain embodiments, it is desirable to group genes that are co-regulated. This allows the comparison of large numbers of profiles. A preferred embodiment for identifying such groups of genes involves clustering algorithms (for reviews of clustering algorithms, *see, e.g.*, Fukunaga, 1990, Statistical Pattern Recognition, 2nd Ed., Academic Press, San Diego; Everitt, 1974, Cluster Analysis, London: Heinemann Educ. Books; Hartigan, 1975, Clustering Algorithms, New York: Wiley; Sneath and Sokal, 1973, Numerical Taxonomy, Freeman; Anderberg, 1973, Cluster Analysis for Applications, Academic Press: New York).

Clustering analysis is useful in helping to reduce complex patterns of thousands of time curves into a smaller set of representative clusters. Some systems allow the clustering and viewing of genes based on sequences. Other systems allow clustering based on other characteristics of the genes, e.g., their level of expression (*see, e.g.*, U.S. Patent No. 6,203,987). Other systems permit clustering of time curves (*see, e.g.* U.S. Patent No. 6,263,287). Cluster analysis can be performed using the hclust routine (*see, e.g.*, "hclust"routine from the software package S-Plus, MathSoft, Inc., Cambridge, Mass.).

In some specific embodiments, genes are grouped according to the degree of co-variation of their transcription, presumably co-regulation, as described in U.S. Patent No. 6,203,987. Groups of genes that have co-varying transcripts are termed "genesets." Cluster analysis or other statistical classification methods can be used to analyze the co-variation of transcription of genes in response to a variety of perturbations, e.g. caused by a disease or a drug. In one specific embodiment, clustering algorithms are applied to expression profiles

to construct a "similarity tree" or "clustering tree" which relates genes by the amount of co-regulation exhibited. Genesets are defined on the branches of a clustering tree by cutting across the clustering tree at different levels in the branching hierarchy.

In some embodiments, a gene expression profile is converted to a projected gene expression profile. The projected gene expression profile is a collection of geneset expression values. The conversion is achieved, in some embodiments, by averaging the level of expression of the genes within each geneset. In some other embodiments, other linear projection processes may be used. The projection operation expresses the profile on a smaller and biologically more meaningful set of coordinates, reducing the effects of measurement errors by averaging them over each cellular constituent sets and aiding biological interpretation of the profile.

Values that can be compared include gross expression levels; averages of expression levels, e.g., from different experiments, different samples from the same subject or samples from different subjects; and ratios of expression levels, e.g., between patients and normal controls.

A variety of other statistical methods are available to assess the degree of relatedness in expression patterns of different genes. Certain statistical methods may be broken into two related portions: metrics for determining the relatedness of the expression pattern of one or more gene, and clustering methods, for organizing and classifying expression data based on a suitable metric (Sherlock, 2000, Curr. Opin. Immunol. 12:201-205; Butte et al., 2000, Pacific Symposium on Biocomputing, Hawaii, World Scientific, p.418-29).

In one embodiment, Pearson correlation may be used as a metric. In brief, for a given gene, each data point of gene expression level defines a vector describing the deviation of the gene expression from the overall mean of gene expression level for that gene across all conditions. Each gene's expression pattern can then be viewed as a series of positive and negative vectors. A Pearson correlation coefficient can then be calculated by comparing the vectors of each gene to each other. An example of such a method is described in Eisen et al. (1998, supra). Pearson correlation coefficients account for the direction of the vectors, but not the magnitudes.

In another embodiment, Euclidean distance measurements may be used as a metric. In these methods, vectors are calculated for each gene in each condition and compared on

the basis of the absolute distance in multidimensional space between the points described by the vectors for the gene.

In a further embodiment, the relatedness of gene expression patterns may be determined by entropic calculations (Butte et al. 2000, supra). Entropy is calculated for each gene's expression pattern. The calculated entropy for two genes is then compared to determine the mutual information. Mutual information is calculated by subtracting the entropy of the joint gene expression patterns from the entropy for calculated for each gene individually. The more different two gene expression patterns are, the higher the joint entropy will be and the lower the calculated mutual information. Therefore, high mutual information indicates a non-random relatedness between the two expression patterns.

The different metrics for relatedness may be used in various ways to identify clusters of genes. In one embodiment, comprehensive pairwise comparisons of entropic measurements will identify clusters of genes with particularly high mutual information. In preferred embodiments, expression patterns for two genes are correlated if the normalized mutual information score is greater than or equal to 0.7, and preferably greater than 0.8, greater than 0.9 or greater than 0.95. In alternative embodiments, a statistical significance for mutual information may be obtained by randomly permuting the expression measurements 30 times and determining the highest mutual information measurement obtained from such random associations. All clusters with a mutual information higher than can be obtained randomly after 30 permutations are statistically significant. In a further embodiment, expression patterns for two genes are correlated if the correlation coefficient is greater than or equal to 0.8, and preferably greater than 0.85, 0.9 or, most preferably greater than 0.95.

In another embodiment, agglomerative clustering methods may be used to identify gene clusters. In one embodiment, Pearson correlation coefficients or Euclidean metrics are determined for each gene and then used as a basis for forming a dendrogram. In one example, genes were scanned for pairs of genes with the closest correlation coefficient. These genes are then placed on two branches of a dendrogram connected by a node, with the distance between the depth of the branches proportional to the degree of correlation. This process continues, progressively adding branches to the tree. Ultimately a tree is formed in which genes connected by short branches represent clusters, while genes connected by longer branches represent genes that are not clustered together. The points in multidimensional space by Euclidean metrics may also be used to generate dendrograms.

In yet another embodiment, divisive clustering methods may be used. For example, vectors are assigned to each gene's expression pattern, and two random vectors are generated. Each gene is then assigned to one of the two random vectors on the basis of probability of matching that vector. The random vectors are iteratively recalculated to generate two centroids that split the genes into two groups. This split forms the major branch at the bottom of a dendrogram. Each group is then further split in the same manner, ultimately yielding a fully branched dendrogram.

In a further embodiment, self-organizing maps (SOM) may be used to generate clusters. In general, the gene expression patterns are plotted in n-dimensional space, using a metric such as the Euclidean metrics described above. A grid of centroids is then placed onto the n-dimensional space and the centroids are allowed to migrate towards clusters of points, representing clusters of gene expression. Finally the centroids represent a gene expression pattern that is a sort of average of a gene cluster. In certain embodiments, SOM may be used to generate centroids, and the genes clustered at each centroid may be further represented by a dendrogram. An exemplary method is described in Tamayo et al., 1999, PNAS 96:2907-12. Once centroids are formed, correlation must be evaluated by one of the methods described supra.

2.2. Other methods for determining gene expression levels

In certain embodiments, it is sufficient to determine the expression of one or only a few genes, as opposed to hundreds or thousands of genes. Although microarrays can be used in these embodiments, various other methods of detection of gene expression are available. This section describes a few exemplary methods for detecting and quantifying mRNA or polypeptide encoded thereby. Where the first step of the methods includes isolation of mRNA from cells, this step can be conducted as described above. Labeling of one or more nucleic acids can be performed as described above.

In one embodiment, mRNA obtained form a sample is reverse transcribed into a first cDNA strand and subjected to PCR, e.g., RT-PCR. House keeping genes, or other genes whose expression does not vary can be used as internal controls and controls across experiments. Following the PCR reaction, the amplified products can be separated by electrophoresis and detected. By using quantitative PCR, the level of amplified product will correlate with the level of RNA that was present in the sample. The amplified samples can also be separated on a agarose or polyacrylamide gel, transferred onto a filter, and the

filter hybridized with a probe specific for the gene of interest. Numerous samples can be analyzed simultaneously by conducting parallel PCR amplification, e.g., by multiplex PCR.

A quantitative PCR technique that can be used is based on the use of TaqMan™ probes. Specific sequence detection occurs by amplification of target sequences in the PE Applied Biosystems 7700 Sequence Detection System in the presence of an oligonucleotide probe labeled at the 5' and 3' ends with a reporter and quencher fluorescent dye, respectively (FQ probe), which anneals between the two PCR primers. Only specific product will be detected when the probe is bound between the primers. As PCR amplification proceeds, the 5'-nuclease activity of Taq polymerase initially cleaves the reporter dye from the probe. The signal generated when the reporter dye is physically separated from the quencher dye is detected by measuring the signal with an attached CCD camera. Each signal generated equals one probe cleaved which corresponds to amplification of one target strand. PCR reactions may be set up using the PE Applied Biosystem TaqMan PCR Core Reagent Kit according to the instructions supplied. This technique is further described, e.g., in U.S. Patent 6,326,462.

In another embodiment, mRNA levels is determined by dotblot analysis and related methods (*see, e.g.*, G. A. Beltz et al., in Methods in Enzymology, Vol. 100, Part B, R. Wu, L. Grossmam, K. Moldave, Eds., Academic Press, New York, Chapter 19, pp. 266-308, 1985). In one embodiment, a specified amount of RNA extracted from cells is blotted (i.e., non-covalently bound) onto a filter, and the filter is hybridized with a probe of the gene of interest. Numerous RNA samples can be analyzed simultaneously, since a blot can comprise multiple spots of RNA. Hybridization is detected using a method that depends on the type of label of the probe. In another dotblot method, one or more probes of one or more genes which are up- or down-regulated during bone or cartilage formation. are attached to a membrane, and the membrane is incubated with labeled nucleic acids obtained from and optionally derived from RNA of a cell or tissue of a subject. Such a dotblot is essentially an array comprising fewer probes than a microarray.

"Dot blot" hybridization gained wide-spread use, and many versions were developed (*see, e.g.*, M. L. M. Anderson and B. D. Young, in Nucleic Acid Hybridization-A Practical Approach, B. D. Hames and S. J. Higgins, Eds., IRL Press, Washington D.C., Chapter 4, pp. 73-111, 1985).

Another format, the so-called "sandwich" hybridization, involves covalently attaching oligonucleotide probes to a solid support and using them to capture and detect

multiple nucleic acid targets (*see, e.g.*, M. Ranki et al., Gene, 21, pp. 77-85, 1983; A. M. Palva, T. M. Ranki, and H. E. Soderlund, in UK Patent Application GB 2156074A, Oct. 2, 1985; T. M. Ranki and H. E. Soderlund in U.S. Pat. No. 4,563,419, Jan. 7, 1986; A. D. B. Malcolm and J. A. Langdale, in PCT WO 86/03782, Jul. 3, 1986; Y. Stabinsky, in U.S. Pat. No. 4,751,177, Jan. 14, 1988; T. H. Adams et al., in PCT WO 90/01564, Feb. 22, 1990; R. B. Wallace et al. 6 Nucleic Acid Res. 11, p. 3543, 1979; and B. J. Connor et al., 80 Proc. Natl. Acad. Sci. USA pp. 278-282, 1983). Multiplex versions of these formats are called "reverse dot blots."

mRNA levels can also be determined by Northern blots. Specific amounts of RNA are separated by gel electrophoresis and transferred onto a filter which is then hybridized with a probe corresponding to the gene of interest. This method, although more burdensome when numerous samples and genes are to be analyzed provides the advantage of being very accurate.

A preferred method for high throughput analysis of gene expression is the serial analysis of gene expression (SAGE) technique, first described in Velculescu et al. (1995) *Science* 270, 484-487. Among the advantages of SAGE is that it has the potential to provide detection of all genes expressed in a given cell type, provides quantitative information about the relative expression of such genes, permits ready comparison of gene expression of genes in two cells, and yields sequence information that can be used to identify the detected genes. Thus far, SAGE methodology has proved itself to reliably detect expression of regulated and nonregulated genes in a variety of cell types (Velculescu et al. (1997) *Cell* 88, 243-251; Zhang et al. (1997) *Science* 276, 1268-1272 and Velculescu et al. (1999) *Nat. Genet.* 23, 387-388).

Techniques for producing and probing nucleic acids are further described, for example, in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989).

Alternatively, the level of expression of one or more genes which are up- or down-regulated during bone or cartilage formation is determined by *in situ* hybridization. In one embodiment, a tissue sample is obtained from a subject, the tissue sample is sliced, and *in situ* hybridization is performed according to methods known in the art, to determine the level of expression of the genes of interest.

In other methods, the level of expression of a gene is detected by measuring the level of protein encoded by the gene. This can be done, e.g., by immunoprecipitation,

ELISA, or immunohistochemistry using an agent, e.g., an antibody, that specifically detects the protein encoded by the gene. Other techniques include Western blot analysis. Immunoassays are commonly used to quantitate the levels of proteins in cell samples, and many other immunoassay techniques are known in the art. The invention is not limited to a particular assay procedure, and therefore is intended to include both homogeneous and heterogeneous procedures. Exemplary immunoassays which can be conducted according to the invention include fluorescence polarization immunoassay (FPIA), fluorescence immunoassay (FIA), enzyme immunoassay (EIA), nephelometric inhibition immunoassay (NIA), enzyme linked immunosorbent assay (ELISA), and radioimmunoassay (RIA). An indicator moiety, or label group, can be attached to the subject antibodies and is selected so as to meet the needs of various uses of the method which are often dictated by the availability of assay equipment and compatible immunoassay procedures. General techniques to be used in performing the various immunoassays noted above are known to those of ordinary skill in the art.

In the case of polypeptides which are secreted from cells, the level of expression of these polypeptides can be measured in biological fluids.

2.3. Data analysis methods

Comparison of the expression levels of one or more genes which are up- or down-regulated in a sample, e.g., of a patient, with reference expression levels, e.g., in normal cells undergoing bone or cartilage formation, is preferably conducted using computer systems. In one embodiment, one or more expression levels are obtained in two cells and these two sets of expression levels are introduced into a computer system for comparison. In a preferred embodiment, one set of one or more expression levels is entered into a computer system for comparison with values that are already present in the computer system, or in computer-readable form that is then entered into the computer system.

In one embodiment, the invention provides a computer readable form of the gene expression profile data of the invention, or of values corresponding to the level of expression of at least one gene which is up- or down-regulated during bone or cartilage formation. The values can be mRNA expression levels obtained from experiments, e.g., microarray analysis. The values can also be mRNA levels normalized relative to a reference gene whose expression is constant in numerous cells under numerous conditions,

e.g., GAPDH. In other embodiments, the values in the computer are ratios of, or differences between, normalized or non-normalized mRNA levels in different samples.

The computer readable medium may comprise values of at least 2, at least 3, at least 5, 10, 20, 50, 100, 200, 500 or more genes, e.g., genes listed in Tables 1, 2, 5 and/or 6. In a preferred embodiment, the computer readable medium comprises at least one expression profile.

Gene expression data can be in the form of a table, such as an Excel table. The data can be alone, or it can be part of a larger database, e.g., comprising other expression profiles, e.g., publicly available database. The computer readable form can be in a computer. In another embodiment, the invention provides a computer displaying the gene expression profile data.

Although the invention provides methods in which the level of expression of a single gene can be compared in two or more cells or tissue samples, in a preferred embodiment, the level of expression of a plurality of genes is compared. For example, the level of expression of at least 2, at least 3, at least 5, 10, 20, 50, 100, 200, 500 or more genes, e.g., genes listed in Tables 1, 2, 5 and/or 6 can be compared. In a preferred embodiment, expression profiles are compared.

In one embodiment, the invention provides a method for determining the similarity between the level of expression of one or more genes which are up- or down-regulated during bone or cartilage formation in a first cell, e.g., a cell of a subject, and that in a second cell. The method preferably comprises obtaining the level of expression of one or more genes which are up- or down-regulated during bone or cartilage formation in a first cell and entering these values into a computer comprising (i) a database including records comprising values corresponding to levels of expression of one or more genes which are up- or down-regulated during bone or cartilage formation in a second cell, and (ii) processor instructions, e.g., a user interface, capable of receiving a selection of one or more values for comparison purposes with data that is stored in the computer. The computer may further comprise a means for converting the comparison data into a diagram or chart or other type of output.

In another embodiment, values representing expression levels of one or more genes which are up- or down-regulated during bone or cartilage formation are entered into a computer system that comprises one or more databases with reference expression levels obtained from more than one cell. For example, the computer may comprise expression

data of diseased, e.g., bone or cartilage cells of an osteoporosis patient, and normal cells. The computer may also comprise expression data of genes at different time points during bone or cartilage formation, e.g., the data set forth in Tables 1, 2, 5 and/or 6. Instructions are provided to the computer, and the computer is capable of comparing the data entered with the data in the computer to determine whether the data entered is more similar to one or the other gene expression data stored in the computer.

In another embodiment, the computer comprises values of expression levels in cells of subjects at different stages of a disease relating to bone or cartilage formation or resorption, and the computer is capable of comparing expression data entered into the computer with the data stored, and produce results indicating to which of the expression data in the computer, the one entered is most similar, such as to determine the stage of the disease in the subject.

In yet another embodiment, the reference expression data in the computer are expression data from cells of one or more subjects having a disease relating to bone or cartilage formation or resorption, which cells are treated *in vivo* or *in vitro* with a drug used for therapy of the disease. Upon entering of expression data of a cell of a subject treated *in vitro* or *in vivo* with the drug, the computer is instructed to compare the data entered with the data in the computer, and to provide results indicating whether the expression data input into the computer are more similar to those of a cell of a subject that is responsive to the drug or more similar to those of a cell of a subject that is not responsive to the drug. Thus, the results indicate whether the subject is likely to respond to the treatment with the drug or unlikely to respond to it.

The reference expression data may also be from cells of subjects responding or not responding to several different treatments, and the computer system indicates a preferred treatment for the subject. Accordingly, the invention provides a method for selecting a therapy for a patient having a disease relating to bone or cartilage formation or resorption, the method comprising: (i) providing the level of expression of one or more genes which are up- or down-regulated during bone or cartilage formation in a diseased cell of the patient; (ii) providing a plurality of reference expression levels, each associated with a therapy, wherein the subject expression levels and each reference expression level has a plurality of values, each value representing the level of expression of a gene that is up- or down-regulated during bone or cartilage formation; and (iii) selecting the reference expression levels most similar to the subject expression levels, to thereby select a therapy

for said patient. In a preferred embodiment step (iii) is performed by a computer. The most similar reference profile may be selected by weighing a comparison value of the plurality using a weight value associated with the corresponding expression data.

In one embodiment, the invention provides a system that comprises a means for receiving gene expression data for one or a plurality of genes; a means for comparing the gene expression data from each of said one or plurality of genes to a common reference frame; and a means for presenting the results of the comparison. This system may further comprise a means for clustering the data.

In another embodiment, the invention provides a computer program for analyzing gene expression data comprising (i) a computer code that receives as input gene expression data for a plurality of genes and (ii) a computer code that compares said gene expression data from each of said plurality of genes to a common reference frame.

The invention also provides a machine-readable or computer-readable medium including program instructions for performing the following steps: (i) comparing a plurality of values corresponding to expression levels of one or more genes which are up- or down-regulated during bone or cartilage formation in a query cell with a database including records comprising reference expression of one or more reference cells and an annotation of the type of cell; and (ii) indicating to which cell the query cell is most similar based on similarities of expression levels.

The relative levels of expression, e.g., abundance of an mRNA, in two biological samples can be scored as a perturbation (relative abundance difference) or as not perturbed (i.e., the relative abundance is the same). For example, a perturbation can be a difference in expression levels between the two sources of RNA of at least a factor of about 25% (RNA from one source is 25% more abundant in one source than the other source), more usually about 50%, even more often by a factor of about 2 (twice as abundant), 3 (three times as abundant) or 5 (five times as abundant). Perturbations can be used by a computer for calculating and expressing comparisons.

Preferably, in addition to identifying a perturbation as positive or negative, it is advantageous to determine the magnitude of the perturbation. This can be carried out, as noted above, by calculating the ratio of the emission of the two fluorophores used for differential labeling, or by analogous methods that will be readily apparent to those of skill in the art.

The computer readable medium may further comprise a pointer to a descriptor of the level of expression or expression profile, e.g., from which source it was obtained, e.g., from which patient it was obtained. A descriptor can reflect the stage of a disease, the therapy that a patient is undergoing or any other descriptions of the source of expression levels.

In operation, the means for receiving gene expression data, the means for comparing the gene expression data, the means for presenting, the means for normalizing, and the means for clustering within the context of the systems of the present invention can involve a programmed computer with the respective functionalities described herein, implemented in hardware or hardware and software; a logic circuit or other component of a programmed computer that performs the operations specifically identified herein, dictated by a computer program; or a computer memory encoded with executable instructions representing a computer program that can cause a computer to function in the particular fashion described herein.

Those skilled in the art will understand that the systems and methods of the present invention may be applied to a variety of systems, including IBM-compatible personal computers running MS-DOS or Microsoft Windows.

The computer may have internal components linked to external components. The internal components may include a processor element interconnected with a main memory. The computer system can be an Intel Pentium®-based processor of 200 MHz or greater clock rate and with 32 MB or more of main memory. The external component may comprise a mass storage, which can be one or more hard disks (which are typically packaged together with the processor and memory). Such hard disks are typically of 1 GB or greater storage capacity. Other external components include a user interface device, which can be a monitor, together with an inputing device, which can be a "mouse", or other graphic input devices, and/or a keyboard. A printing device can also be attached to the computer.

Typically, the computer system is also linked to a network link, which can be part of an Ethernet link to other local computer systems, remote computer systems, or wide area communication networks, such as the Internet. This network link allows the computer system to share data and processing tasks with other computer systems.

Loaded into memory during operation of this system are several software components, which are both standard in the art and special to the instant invention. These

software components collectively cause the computer system to function according to the methods of this invention. These software components are typically stored on a mass storage. A software component represents the operating system, which is responsible for managing the computer system and its network interconnections. This operating system can be, for example, of the Microsoft Windows' family, such as Windows 95, Windows 98, or Windows NT. A software component represents common languages and functions conveniently present on this system to assist programs implementing the methods specific to this invention. Many high or low level computer languages can be used to program the analytic methods of this invention. Instructions can be interpreted during run-time or compiled. Preferred languages include C/C++, and JAVA®. Most preferably, the methods of this invention are programmed in mathematical software packages which allow symbolic entry of equations and high-level specification of processing, including algorithms to be used, thereby freeing a user of the need to procedurally program individual equations or algorithms. Such packages include Matlab from Mathworks (Natick, Mass.), Mathematica from Wolfram Research (Champaign, Ill.), or S-Plus from Math Soft (Cambridge, Mass.). Accordingly, a software component represents the analytic methods of this invention as programmed in a procedural language or symbolic package. In a preferred embodiment, the computer system also contains a database comprising values representing levels of expression of one or more genes which are up- or down-regulated during bone or cartilage formation. The database may contain one or more expression profiles of genes which are up- or down-regulated during bone or cartilage formation in different cells.

In an exemplary implementation, to practice the methods of the present invention, a user first loads expression data into the computer system. These data can be directly entered by the user from a monitor and keyboard, or from other computer systems linked by a network connection, or on removable storage media such as a CD-ROM or floppy disk or through the network. Next the user causes execution of expression profile analysis software which performs the steps of comparing and, e.g., clustering co-varying genes into groups of genes.

In another exemplary implementation, expression profiles are compared using a method described in U.S. Patent No. 6,203,987. A user first loads expression profile data into the computer system. Geneset profile definitions are loaded into the memory from the storage media or from a remote computer, preferably from a dynamic geneset database system, through the network. Next the user causes execution of projection software which

performs the steps of converting expression profile to projected expression profiles. The projected expression profiles are then displayed.

In yet another exemplary implementation, a user first leads a projected profile into the memory. The user then causes the loading of a reference profile into the memory. Next, the user causes the execution of comparison software which performs the steps of objectively comparing the profiles.

3. Exemplary diagnostic and prognostic compositions and devices of the invention

Any composition and device (e.g., an array) for use in the above-described methods are within the scope of the invention.

In one embodiment, the invention provides a composition comprising a plurality of detection agents for detecting expression of genes which are up- or down-regulated during bone or cartilage formation. In a preferred embodiment, the composition comprises at least 2, preferably at least 3, 5, 10, 20, 50, or 100 different detection agents, such as to genes listed in Tables 1, 2, 5 and/or 6. In certain embodiments, the composition comprises at most about 1000, 500, 300, 100, 50, 30, 10, 5 or 3 detection agents. Certain composition may comprise no more than about 1, 2, 3, 5, or 10 detection agents of genes which are not listed in Tables 1, 2, 5 and/or 6. In certain compositions, less than about 1%, 3%, 5%, 10%, 30% or 50% of the detection agents are to genes that are not listed in Tables 1, 2, 5 and/or 6. A detection agent can be a nucleic acid probe, e.g., DNA or RNA, or it can be a polypeptide, e.g., as antibody that binds to the polypeptide encoded by a gene that is up- or down-regulated during bone or cartilage formation. The probes can be present in equal amount or in different amounts in the solution.

A nucleic acid probe can be at least about 10 nucleotides long, preferably at least about 15, 20, 25, 30, 50, 100 nucleotides or more, and can comprise the full length gene. Preferred probes are those that hybridize specifically to genes listed in any of Tables 1, 2, 5 and/or 6. If the nucleic acid is short (i.e., 20 nucleotides or less), the sequence is preferably perfectly complementary to the target gene (i.e., a gene that is up- or down-regulated during bone or cartilage formation), such that specific hybridization can be obtained. However, nucleic acids, even short ones that are not perfectly complementary to the target gene can also be included in a composition of the invention, e.g., for use as a negative control. Certain compositions may also comprise nucleic acids that are complementary to, and capable of detecting, an allele of a gene.

In a preferred embodiment, the invention provides nucleic acids which hybridize under high stringency conditions of 0.2 to 1 x SSC at 65 °C followed by a wash at 0.2 x SSC at 65 °C to genes which are up- or down-regulated during bone or cartilage formation. In another embodiment, the invention provides nucleic acids which hybridize under low stringency conditions of 6 x SSC at room temperature followed by a wash at 2 x SSC at room temperature. Other nucleic acids probes hybridize to their target in 3 x SSC at 40 or 50 °C, followed by a wash in 1 or 2 x SSC at 20, 30, 40, 50, 60, or 65 °C.

Nucleic acids which are at least about 80%, preferably at least about 90%, even more preferably at least about 95% and most preferably at least about 98% identical to genes which are up- or down-regulated during bone or cartilage formation or cDNAs thereof, complements thereof, fragments and variants are also within the scope of the invention.

Nucleic acid probes can be obtained by, e.g., polymerase chain reaction (PCR) amplification of gene segments from genomic DNA, cDNA (e.g., by RT-PCR), or cloned sequences. PCR primers are chosen, based on the known sequence of the genes or cDNA, that result in amplification of unique fragments. Computer programs can be used in the design of primers with the required specificity and optimal amplification properties. *See, e.g.*, Oligo version 5.0 (National Biosciences). Factors which apply to the design and selection of primers for amplification are described, for example, by Rylchik, W. (1993) "Selection of Primers for Polymerase Chain Reaction," in Methods in Molecular Biology, Vol. 15, White B. ed., Humana Press, Totowa, N.J. Sequences can be obtained from GenBank or other public sources.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16: 3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Nat. Acad. Sci. U.S.A. 85: 7448-7451), etc. In another embodiment, the oligonucleotide is a 2'-0-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15: 6131-6148), or a chimeric RNA-DNA analog (Inoue et al., 1987, FEBS Lett. 215: 327-330).

"Rapid amplification of cDNA ends," or RACE, is a PCR method that can be used for amplifying cDNAs from a number of different RNAs. The cDNAs may be ligated to an

oligonucleotide linker and amplified by PCR using two primers. One primer may be based on sequence from the instant nucleic acids, for which full length sequence is desired, and a second primer may comprise a sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this method is reported in PCT Pub. No. WO 97/19110.

In another embodiment, the invention provides a composition comprising a plurality of agents which can detect a polypeptide encoded by a gene that is up- or down-regulated during bone or cartilage formation. An agent can be, e.g., an antibody. Antibodies to polypeptides described herein can be obtained commercially, or they can be produced according to methods known in the art.

The probes can be attached to a solid support, such as paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate, such as those further described herein. For example, probes of genes which are up- or down-regulated during bone or cartilage formation can be attached covalently or non covalently to membranes for use, e.g., in dotblots, or to solids such as to create arrays, e.g., microarrays. Exemplary solid surfaces, e.g., arrays, comprise probes corresponding to all or a portion of the genes listed in Tables 1, 2, 5 and/or 6. Solid surfaces may comprise at least about 1, 2, 3, 5, 10, 20, 30, or 100 probes corresponding to genes listed in Tables 1, 2, 5 and/or 6. In certain embodiments, solid surfaces comprise less than about 1, 2, 3, 5, 10, 20, 30, or 100 probes corresponding to genes that are not listed in Tables 1, 2, 5 and/or 6. In certain solid surfaces, less than about 1%, 2%, 3%, 5%, 10%, 20%, 30%, or 50% of the probes are probes that correspond to genes that are not listed in any of Tables 1, 2, 5 and/or 6.

The invention also provides computer-readable media and computers comprising expression values of all or a portion of the genes set forth in Tables 1, 2, 5 and/or 6 during bone and cartilage development, such as the values set forth in Tables 1, 2, 5 and/or 6. The media and computers may comprise at least about 1, 2, 3, 5, 10, 20, 30, or 100 values of genes listed in Tables 1, 2, 5 and/or 6. In certain embodiments, media and computers comprise less than about 1, 2, 3, 5, 10, 20, 30, or 100 values of genes that are not listed in Tables 1, 2, 5 and/or 6. In certain media and computers, less than about 1%, 2%, 3%, 5%, 10%, 20%, 30%, or 50% of the values correspond to genes that are not listed in Tables 1, 2, 5 and/or 6.

Methods for preparing compositions and devices, e.g., computer readable media, are also within the scope of the invention.

4. Therapeutic methods and compositions

Up- or down-regulation of genes which have been shown to be down- and up-regulated during bone formation, respectively, can be used as a therapeutic method in various situations, e.g., diseases relating to bone and cartilage formation, such as osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; inflammatory diseases, such as rheumatoid arthritis and osteoarthritis; periondontal disease or other teeth related diseases; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; wound healing and related tissue repair (e.g., burns, incisions and ulcers); healing of fractures, e.g., in closed and open fracture reduction; improved fixation of artificial joints; repair of congenital, trauma induced, or oncologic resection induced craniofacial defects; tooth repair processes and plastic, e.g., cosmetic plastic, surgery.

Accordingly, in certain diseases, e.g., osteoporosis, which can be treated by stimulating bone or cartilage formation, the invention provides methods for stimulating bone or cartilage formation. In other diseases, e.g., osteodystrophy, osteohypertrophy, osteoma, osteoblastoma and cancers, which can be treated by inhibiting bone or cartilage formation, the invention provides methods for inhibiting bone or cartilage formation.

Certain genes have been shown herein to be expressed maximally in differentiated bone cells (see, e.g., genes represented in bold and italics in Table 1). Such genes are likely to be markers of osteoclast formation, differentiation or activity. Thus, inhibiting the expression of one or more of these genes or reducing the activity of level of the protein encoded thereby, will reduce osteoclast activity, and could thus be used in treating diseases relating to excessive osteoclast activity, e.g., osteopenia, osteoporosis and erosion associated with arthritis.

In other embodiments, the invention is used for stimulating *in vitro* formation of bone or cartilage that can then be implanted into subjects.

In one embodiment, a therapeutic method includes increasing or decreasing the level of expression of one or more genes whose expression is abnormally low or high, respectively, relatively to that in a normal subject. For example, the invention may comprise first determining the level of expression of one or more genes that are up- or down-regulated during bone or cartilage formation, e.g., genes in any of the Tables

described herein, and then bringing the level of expression of the genes whose level of expression differs from the control to about the level in the control.

Gene expression may be normalized, i.e., brought to within a similar level relative to a control, by various ways. For example, gene expression may be normalized by administering the protein that is encoded by the gene; by administering a nucleic acid encoding the protein that is encoded by the gene; or by stimulating expression of the gene. Reducing gene expression can be achieved, e.g., by administration of antisense, siRNA, ribozymes or aptamers directed to the gene or antibodies or other molecules that bind and, e.g., inactivate the protein encoded by the gene.

In certain embodiments, osteogenic, cartilage-inducing or bone inducing factors can be co-administered together with a gene-specific therapeutic to a subject. For example, a growth or differentiation factor or bone morphogenetic protein, e.g., BMP-2 can be co-administered. Other factors that can be co-administered include those described in European patent applications 148,155 and 169,016.

4.1. Methods for confirming that modulation of the expression of a gene improves a disease relating to bone or cartilage formation or resorption

In one embodiment, the effect of up- or down-regulating the level of expression of a gene which is down- or up-regulated, respectively, in a cell of a subject having a disease relating to bone or cartilage formation or resorption can be confirmed by phenotypic analysis of the cell characteristic of the disease, in particular by determining whether the cell adopts a phenotype that is more reminiscent of that of a normal cell than that of a cell characteristic of the disease relating to bone or cartilage formation or resorption. A "cell characteristic of a disease" also referred to as a "diseased cell" refers to a cell of a subject having a disease, which cell is affected by the disease, and is therefore different from the corresponding cell in a non-diseased subject. For example a cell characteristic of cancer is a cancer cell or tumor cell.

The effect on the cell can also be confirmed by measuring the level of expression of one or more genes which are up- or down-regulated during bone or cartilage formation, and preferably at least about 10, or at least about 100 genes which are up- or down-regulated during bone or cartilage formation. In a preferred embodiment, the level of expression of a gene is modulated, and the level of expression of at least one gene that is up- or down-regulated during bone or cartilage formation is determined, e.g., by using a microarray

having probes to the one or more genes. If the normalization of expression of the gene results in at least some normalization of the gene expression profile in the diseased cell, then normalizing the expression of the gene in the subject having the disease is expected to improve the disease. The term "normalization of the expression of a gene in a diseased cell" refers to bringing the level of expression of that gene in the diseased cell to a level that is similar to that in the corresponding normal cell. "Normalization of the gene expression profile in a diseased cell" refers to bringing the expression profile in a diseased cell essentially to that in the corresponding non-diseased cell. If, however, the normalization of expression of the gene does not result in at least some normalization of the gene expression profile in the diseased cell, normalizing the expression of the gene in a subject having a disease relating to bone or cartilage formation or resorption. is not expected to improve the disease. In certain embodiments, the expression level of two or more genes which are up- or down-regulated during bone or cartilage formation is modulated and the effect on the diseased cell is determined.

A preferred cell for use in these assays is a cell characteristic of a disease relating to bone or cartilage formation or resorption that can be obtained from a subject and, e.g., established as a primary cell culture. The cell can be immortalized by methods known in the art, e.g., by expression of an oncogene or large T antigen of SV40. Alternatively, cell lines corresponding to such a diseased cell can be used. Examples include RAW cells and THP1 cells. However, prior to using such cell lines, it may be preferably to confirm that the gene expression profile of the cell line corresponds essentially to that of a cell characteristic of a disease related to bone or cartilage formation or resorption. This can be done as described in details herein.

Modulating the expression of a gene in a cell can be achieved, e.g., by contacting the cell with an agent that increases the level of expression of the gene or the activity of the polypeptide encoded by the gene. Increasing the level of a polypeptide in a cell can also be achieved by transfecting the cell, transiently or stably, with a nucleic acid encoding the polypeptide. Decreasing the expression of a gene in a cell can be achieved by inhibiting transcription or translation of the gene or RNA, e.g., by introducing antisense nucleic acids, ribozymes or siRNAs into the cells, or by inhibiting the activity of the polypeptide encoded by the gene, e.g., by using antibodies or dominant negative mutants. These methods are further described below in the context of therapeutic methods.

A nucleic acid encoding a particular polypeptide can be obtained, e.g., by RT-PCR from a cell that is known to express the gene. Primers for the RT-PCR can be derived from the nucleotide sequence of the gene encoding the polypeptide. The nucleotide sequence of the gene is available, e.g., in GenBank or in the publications. GenBank Accession numbers of the genes listed in Tables 1, 2, 5 and/or 6 are provided in the tables. Amplified DNA can then be inserted into an expression vector, according to methods known in the art and transfected into diseased cells of a disease related to bone or cartilage formation or resorption. In a control experiment, normal counterpart cells can also be transfected. The level of expression of the polypeptide in the transfected cells can be determined, e.g., by electrophoresis and staining of the gel or by Western blot using an a agent that binds the polypeptide, e.g., an antibody. The level of expression of one or more genes which are up- or down-regulated during bone or cartilage formation. can then be determined in the transfected cells having elevated levels of the polypeptide. In a preferred embodiment, the level of expression is determined by using a microarray. For example, RNA is extracted from the transfected cells, and used as target DNA for hybridization to a microarray, as further described herein.

These assays will allow the identification of genes which are up- or down-regulated during bone or cartilage formation that can be used as therapeutic targets for developing therapeutics for diseases relating to bone or cartilage formation or resorption.

4.2. Therapeutic methods

4.2.1. Methods for reducing expression of a gene or the activity or level of the protein encoded thereby in a patient

Genes that are expressed at higher levels in diseased cells of subjects having a disease relating to bone or cartilage formation or resorption relative to their expression level in a normal cell undergoing bone or cartilage formation may be used as therapeutic targets for treating the disease. For example, it is possible to treat such a disease by decreasing the level of the polypeptides in diseased cells. Similarly, where bone or cartilage formation is undesired, it may be inhibited by blocking or reducing the expression of a gene or the activity or level of the encoded polypeptide that is modulated, e.g., up-regulated, during normal bone or cartilage formation. Bone and cartilage formation may also be stimulated by blocking or reducing the expression of a gene or the activity or level of the encoded

polypeptide that is modulated, e.g., down-regulated, during normal bone or cartilage formation.

(i) Antisense nucleic acids

One method for decreasing the level of expression of a gene is to introduce into the cell antisense molecules which are complementary to at least a portion of the gene or RNA of the gene. An "antisense"nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific (e.g., non-poly A) portion of the target RNA, for example its translation initiation region, by virtue of some sequence complementarity to a coding and/or non-coding region. The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof, which can be directly administered in a controllable manner to a cell or which can be produced intracellularly by transcription of exogenous, introduced sequences in controllable quantities sufficient to perturb translation of the target RNA.

Preferably, antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides (ranging from 6 to about 200 oligonucleotides). In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, or agents facilitating transport across the cell membrane (*see, e.g.*, Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86: 6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84: 648-652: PCT Publication No. WO 88/09810, published Dec. 15, 1988), hybridization-triggered cleavage agents (*see, e.g.*, Krol et al., 1988, BioTechniques 6: 958-976) or intercalating agents (*see, e.g.*, Zon, 1988, Pharm. Res. 5: 539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position on its structure with constituents generally known in the art. For example, the antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil,

dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl)uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the oligonucleotide is a 2-α-anomeric oligonucleotide. An α-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent transport agent, hybridization-triggered cleavage agent, etc. An antisense molecule can be a "peptide nucleic acid" (PNA). PNA refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of a target RNA species. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense

nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a target RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex. The amount of antisense nucleic acid that will be effective in the inhibiting translation of the target RNA can be determined by standard assay techniques.

The synthesized antisense oligonucleotides can then be administered to a cell in a controlled manner. For example, the antisense oligonucleotides can be placed in the growth environment of the cell at controlled levels where they may be taken up by the cell. The uptake of the antisense oligonucleotides can be assisted by use of methods well known in the art.

In an alternative embodiment, the antisense nucleic acids of the invention are controllably expressed intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known in the art to act in a cell of interest. Such promoters can be inducible or constitutive. Most preferably, promoters are controllable or inducible by the administration of an exogenous moiety in order to achieve controlled expression of the antisense oligonucleotide. Such controllable promoters include the Tet promoter. Other usable promoters for mammalian cells include, but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290: 304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, Cell 22: 787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78: 1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296: 39-42), etc.

Antisense therapy for a variety of cancers is in clinical phase and has been discussed extensively in the literature. Reed reviewed antisense therapy directed at the Bcl-2 gene in tumors; gene transfer-mediated overexpression of Bcl-2 in tumor cell lines conferred resistance to many types of cancer drugs. (Reed, J.C., *N.C.I.* (1997) *89*:988-990). The potential for clinical development of antisense inhibitors of *ras* is discussed by Cowsert, L.M., *Anti-Cancer Drug Design* (1997) *12*:359-371. Additional important antisense targets include leukemia (Geurtz, A.M., *Anti-Cancer Drug Design* (1997) *12*:341-358); human C-ref kinase (Monia, B.P., *Anti-Cancer Drug Design* (1997) *12*:327-339); and protein kinase C (McGraw *et al., Anti-Cancer Drug Design* (1997) *12*:315-326.

(ii) Ribozymes

In another embodiment, the level of a particular mRNA or polypeptide in a cell is reduced by introduction of a ribozyme into the cell or nucleic acid encoding such. Ribozyme molecules designed to catalytically cleave mRNA transcripts can also be introduced into, or expressed, in cells to inhibit expression of the gene (*see, e.g.*, Sarver *et al.*, 1990, *Science* 247:1222-1225 and U.S. Patent No. 5,093,246). One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme is disclosed in Usman *et al., Current Opin. Struct. Biol.* (1996) *6*:527-533. Usman also discusses the therapeutic uses of ribozymes. Ribozymes can also be prepared and used as described in Long *et al., FASEB J.* (1993) *7*:25; Symons, *Ann. Rev. Biochem.* (1992) *61*:641; Perrotta *et al., Biochem.* (1992) *31*:16-17; Ojwang *et al., Proc. Natl. Acad. Sci. (USA)* (1992) *89*:10802-10806; and U.S. Patent No. 5,254,678. Ribozyme cleavage of HIV-I RNA is described in U.S. Patent No. 5,144,019; methods of cleaving RNA using ribozymes is described in U.S. Patent No. 5,116,742; and methods for increasing the specificity of ribozymes are described in U.S. Patent No. 5,225,337 and Koizumi *et al., Nucleic Acid Res.* (1989) *17*:7059-7071. Preparation and use of ribozyme fragments in a hammerhead structure are also described by Koizumi *et al., Nucleic Acids Res.* (1989) *17*:7059-7071. Preparation and use of ribozyme fragments in a hairpin structure are described by Chowrira and Burke, *Nucleic Acids Res.* (1992) *20*:2835. Ribozymes can also be made by rolling transcription as described in Daubendiek and Kool, *Nat. Biotechnol.* (1997) *15(3)*:273-277.

(iii) siRNAs

Another method for decreasing or blocking gene expression is by introducing double stranded small interfering RNAs (siRNAs), which mediate sequence specific mRNA

degradation. RNA interference (RNAi) is the process of sequence-specific, post-transcriptional gene silencing in animals and plants, initiated by double-stranded RNA (dsRNA) that is homologous in sequence to the silenced gene. *In vivo*, long dsRNA is cleaved by ribonuclease III to generate 21- and 22-nucleotide siRNAs. It has been shown that 21-nucleotide siRNA duplexes specifically suppress expression of endogenous and heterologous genes in different mammalian cell lines, including human embryonic kidney (293) and HeLa cells (Elbashir et al. Nature 2001 ;411(6836):494-8).

(iv) Triplex formation

Gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the target gene (i.e., the gene promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally, Helene, C. 1991, Anticancer Drug Des., 6(6):569-84; Helene, C., et al., 1992, Ann, N.Y. Accad. Sci., 660:27-36; and Maher, L.J., 1992, Bioassays 14(12):807-15).

(v) Aptamers

In a further embodiment, RNA aptamers can be introduced into or expressed in a cell. RNA aptamers are specific RNA ligands for proteins, such as for Tat and Rev RNA (Good et al., 1997, Gene Therapy 4: 45-54) that can specifically inhibit their translation.

(vi) Dominant negative mutants

Another method of decreasing the biological activity of a polypeptide is by introducing into the cell a dominant negative mutant. A dominant negative mutant polypeptide will interact with a molecule with which the polypeptide normally interacts, thereby competing for the molecule, but since it is biologically inactive, it will inhibit the biological activity of the polypeptide. A dominant negative mutant can be created by mutating the substrate-binding domain, the catalytic domain, or a cellular localization domain of the polypeptide. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants. *See* Herskowitz, *Nature* (1987) *329*:219-222.

(vi) Use of agents inhibiting transcription or polypeptide activity

In another embodiment, a compound decreasing the expression of the gene of interest or the activity of the polypeptide is administered to a subject having a disease

relating to bone or cartilage formation or resorption, such that the level or activity of the polypeptide in the diseased cells decreases, and the disease is improved. Compounds may be known in the art or can be identified as further described herein. For example, where the gene encodes a polypeptide that is a protease, the activity of the protease can be inhibited, e.g., by a compound that binds an active site of the enzyme, by a compound that inhibits the interaction of the protease with its target, or by a compound that decreases the stability of the protease.

4.2.2. Methods for increasing the expression of a gene or the activity or level of the protein encoded thereby in a patient

Genes which are expressed at lower levels in diseased cells of subjects having a disease relating to bone or cartilage formation or resorption relative to their expression level in a normal cell undergoing bone or cartilage formation may be used as therapeutic targets for treating such diseases. For example, it may be possible to treat such a disease by increasing the level of the polypeptides in diseased cells. Similarly, where on wishes to stimulate bone formation, one may increase the level of expression of a gene or the activity or level of protein encoded by the gene that is modulated, e.g., up-regulated, during bone or cartilage formation. If one wishes to inhibit bone or cartilage formation, one may increase the level of expression of a gene or the activity or level of protein encoded by the gene that is modulated, e.g., down-regulated, during bone or cartilage formation.

(i) Administration of a nucleic acid encoding a polypeptide of interest to a subject

In one embodiment, a nucleic acid encoding a polypeptide of interest, or an equivalent thereof, such as a functionally active fragment of the polypeptide, is administered to a subject, such that the nucleic acid arrives at the site of the diseased cells, traverses the cell membrane and is expressed in the diseased cell.

A nucleic acid encoding a polypeptide of interest can be obtained as described herein, e.g., by RT-PCR, or from publicly available DNA clones. It may not be necessary to express the full length polypeptide in a cell of a subject, and a functional fragment thereof may be sufficient. Similarly, it is not necessary to express a polypeptide having an amino acid sequence that is identical to that of the wild-type polypeptide. Certain amino acid deletions, additions and substitutions are permitted, provided that the polypeptide retains most of its biological activity. For example, it is expected that polypeptides having conservative amino acid substitutions will have the same activity as the polypeptide.

Polypeptides that are shorter or longer than the wild-type polypeptide or which contain from one to 20 amino acid deletions, insertions or substitutions and which have a biological activity that is essentially identical to that of the wild-type polypeptide are referred to herein as "equivalents of the polypeptide." Equivalent polypeptides also include polypeptides having an amino acid sequence which is at least 80%, preferably at least about 90%, even more preferably at least about 95% and most preferably at least 98% identical or similar to the amino acid sequence of the wild-type polypeptide.

Determining which portion of the polypeptide is sufficient for improving a disease relating to bone or cartilage formation or which polypeptides derived from the polypeptide are "equivalents" which can be used for treating the disease, can be done in *in vitro* assays. For example, expression plasmids encoding various portions of the polypeptide can be transfected into cells, e.g., diseased cells of patients, and the effect of the expression of the portion of the polypeptide in the cells can be determined, e.g., by visual inspection of the phenotype of the cell or by obtaining the expression profile of the cell, as further described herein.

Any means for the introduction of polynucleotides into mammals, human or non-human, may be adapted to the practice of this invention for the delivery of the various constructs of the invention into the intended recipient. In one embodiment of the invention, the DNA constructs are delivered to cells by transfection, i.e., by delivery of "naked" DNA or in a complex with a colloidal dispersion system. A colloidal system includes macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a lipid-complexed or liposome-formulated DNA. In the former approach, prior to formulation of DNA, e.g., with lipid, a plasmid containing a transgene bearing the desired DNA constructs may first be experimentally optimized for expression (e.g., inclusion of an intron in the 5' untranslated region and elimination of unnecessary sequences (Felgner, et al., Ann NY Acad Sci 126-139, 1995). Formulation of DNA, e.g. with various lipid or liposome materials, may then be effected using known methods and materials and delivered to the recipient mammal. See, e.g., Canonico et al, Am J Respir Cell Mol Biol 10:24-29, 1994; Tsan et al, Am J Physiol 268; Alton et al., Nat Genet. 5:135-142, 1993 and U.S. patent No. 5,679,647 by Carson et al.

The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-

specific, cell-specific, and organelle-specific. Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to cells of the reticulo-endothelial system (RES) in organs, which contain sinusoidal capillaries. Active targeting, on the other hand, involves alteration of the liposome by coupling the liposome to a specific ligand such as a monoclonal antibody, sugar, glycolipid, or protein, or by changing the composition or size of the liposome in order to achieve targeting to organs and cell types other than the naturally occurring sites of localization.

The surface of the targeted delivery system may be modified in a variety of ways. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in stable association with the liposomal bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand. Naked DNA or DNA associated with a delivery vehicle, e.g., liposomes, can be administered to several sites in a subject (see below).

In a preferred method of the invention, the DNA constructs are delivered using viral vectors. The transgene may be incorporated into any of a variety of viral vectors useful in gene therapy, such as recombinant retroviruses, adenovirus, adeno-associated virus (AAV), and herpes simplex virus-1, or recombinant bacterial or eukaryotic plasmids. While various viral vectors may be used in the practice of this invention, AAV- and adenovirus-based approaches are of particular interest. Such vectors are generally understood to be the recombinant gene delivery system of choice for the transfer of exogenous genes *in vivo*, particularly into humans.

It is possible to limit the infection spectrum of viruses by modifying the viral packaging proteins on the surface of the viral particle (see, for example PCT publications WO93/25234, WO94/06920, and WO94/11524). For instance, strategies for the modification of the infection spectrum of viral vectors include: coupling antibodies specific for cell surface antigens to envelope protein (Roux et al., (1989) PNAS USA 86:9079-9083; Julan et al., (1992) J. Gen Virol 73:3251-3255; and Goud et al., (1983) Virology 163:251-254); or coupling cell surface ligands to the viral envelope proteins (Neda et al., (1991) J. Biol. Chem. 266:14143-14146). Coupling can be in the form of the chemical cross-linking with a protein or other variety (e.g. lactose to convert the env protein to an asialoglycoprotein), as well as by generating fusion proteins (e.g. single-chain antibody/env fusion proteins). This technique, while useful to limit or otherwise direct the infection to

certain tissue types, and can also be used to convert an ecotropic vector in to an amphotropic vector.

The expression of a polypeptide of interest or equivalent thereof in cells of a patient to which a nucleic acid encoding the polypeptide was administered can be determined, e.g., by obtaining a sample of the cells of the patient and determining the level of the polypeptide in the sample, relative to a control sample. The successful administration to a patient and expression of the polypeptide or an equivalent thereof in the cells of the patient can be monitored by determining the expression of at least one gene that is up- or down-regulated during bone or cartilage formation, and preferably by determining an expression profile including most of the genes which are up- or down-regulated during bone or cartilage formation, as described herein.

(ii) Administration of a polypeptide of interest to a subject

In another embodiment, a polypeptide of interest, or an equivalent or variant thereof, e.g., a functional fragment thereof, is administered to the subject such that it reaches the diseased cells of a disease related to bone or cartilage formation or resorption, and traverses the cellular membrane. Polypeptides can be synthesized in prokaryotes or eukaryotes or cells thereof and purified according to methods known in the art. For example, recombinant polypeptides can be synthesized in human cells, mouse cells, rat cells, insect cells, yeast cells, and plant cells. Polypeptides can also be synthesized in cell free extracts, e.g., reticulocyte lysates or wheat germ extracts. Purification of proteins can be done by various methods, e.g., chromatographic methods (*see, e.g.*, Robert K Scopes "Protein Purification: Principles and Practice" Third Ed. Springer-Verlag, N.Y. 1994). In one embodiment, the polypeptide is produced as a fusion polypeptide comprising an epitope tag consisting of about six consecutive histidine residues. The fusion polypeptide can then be purified on a Ni^{++} column. By inserting a protease site between the tag and the polypeptide, the tag can be removed after purification of the peptide on the Ni^{++} column. These methods are well known in the art and commercial vectors and affinity matrices are commercially available.

Administration of polypeptides can be done by mixing them with liposomes, as described above. The surface of the liposomes can be modified by adding molecules that will target the liposome to the desired physiological location.

In one embodiment, a polypeptide is modified so that its rate of traversing the cellular membrane is increased. For example, the polypeptide can be fused to a second

peptide which promotes "transcytosis," e.g., uptake of the peptide by cells. In one embodiment, the peptide is a portion of the HIV transactivator (TAT) protein, such as the fragment corresponding to residues 37 -62 or 48-60 of TAT, portions which are rapidly taken up by cell *in vitro* (Green and Loewenstein, (1989) Cell 55:1179-1188). In another embodiment, the internalizing peptide is derived from the Drosophila antennapedia protein, or homologs thereof. The 60 amino acid long homeodomain of the homeo-protein antennapedia has been demonstrated to translocate through biological membranes and can facilitate the translocation of heterologous polypeptides to which it is couples. Thus, polypeptides can be fused to a peptide consisting of about amino acids 42-58 of Drosophila antennapedia or shorter fragments for transcytosis. See for example Derossi et al. (1996) J Biol Chem 271:18188-18193; Derossi et al. (1994) J Biol Chem 269:10444-10450; and Perez et al. (1992) J Cell Sci 102:717-722.

(iii) *Use of agents stimulating transcription or polypeptide activity*

In another embodiment, a pharmaceutical composition comprising a compound that stimulates the level of expression of a gene of interest or the activity of the polypeptide in a cell is administered to a subject, such that the level of expression of the gene or polypeptide level or activity in the diseased cells is increased or even restored, and the disease is improving in the subject. Compounds may be known in the art or can be identified as further described herein. Compounds may increase the activity of a polypeptide by stabilizing the polypeptide.

4.3. Drug design and discovery of therapeutics

The invention further provides methods for identifying therapeutics that modulate bone and cartilage formation. For example, therapeutics that inhibit bone or cartilage formation can be identified by treating mesenchymal precursor cells with an agent, such as a bone mophogenetic protein, e.g., BMP-2, in the presence or absence of a test compound and determining whether bone or cartilage formation is inhibited or not by the presence of the test compound. The effect on bone or cartilage formation can be measured by determining the level of expression of one or more genes that are up- or down-regulated during bone or cartilage formation, e.g., genes set forth in Tables 1, 2, 5 and/or 6. The assay that is described in the Examples can be used in such assays.

In another embodiment, therapeutics which stimulate bone formation can be identified by contacting mesenchymal precursor cells with a test compound and

determining whether bone or cartilage formation is stimulated in the presence of the test compound. A positive control for this assay can be cells treated with an agent known to cause bone or cartilage formation or differentiation, such as BMP-2. Alternatively, gene expression levels can be measured over a time course and the levels compared to those set forth in Tables 1, 2, 5 and/or 6.

As described above, genes whose modulation of expression improve a disease related to bone or cartilage formation or resorption can be used as targets in drug design and discovery. For example, assays can be conducted to identify molecules that modulate the expression and or activity of genes which are up- or down-regulated during bone or cartilage formation.

In one embodiment, the invention provides methods for identifying an agonist or antagonist of a polypeptide, comprising contacting the polypeptide with a test compound under essentially physiological conditions, and determining whether the test compound binds to the polypeptide or not. In another embodiment, the invention provides a method for identifying an agonist or antagonist of a polypeptide, comprising contacting the polypeptide with a test compound under essentially physiological conditions; and determining a biological activity of the polypeptide in the presence of the test compound, wherein a higher or lower biological activity in the presence relative to the absence of the test compound indicates that the test compound is an agonist or antagonist of the polypeptide. Other assays may be based on a change in the polypeptide, e.g., a change in its phosphorylation level.

In another embodiment, an agent that modulates the expression of a gene that is up- or down-regulated during bone or cartilage formation is identified by contacting cells expressing the gene with one or more test compounds, and monitoring the level of expression of the gene, e.g., by directly or indirectly determining the level of the protein encoded by the gene. Alternatively, compounds which modulate the expression of the gene can be identified by conducting assays using the promoter region of a gene and screening for compounds which modify binding of proteins to the promoter region. The nucleotide sequence of the promoter may be described in a publication or available in GenBank. Alternatively, the promoter region of the gene can be isolated, e.g., by screening a genomic library with a probe corresponding to the gene. Such methods are known in the art.

Inhibitors of the polypeptide can also be agents which bind to the polypeptide, and thereby prevent it from functioning normally, or which degrades or causes the polypeptide

to be degraded. For example, such an agent can be an antibody or derivative thereof which interacts specifically with the polypeptide. Preferred antibodies are monoclonal antibodies, humanized antibodies, human antibodies, and single chain antibodies. Such antibodies can be prepared and tested as known in the art.

If a polypeptide of interest binds to another polypeptide, drugs can be developed which modulate the activity of the polypeptide by modulating its binding to the other polypeptide (referred to herein as "binding partner"). Cell-free assays can be used to identify compounds which are capable of interacting with the polypeptide or binding partner, to thereby modify the activity of the polypeptide or binding partner. Such a compound can, e.g., modify the structure of the polypeptide or binding partner and thereby effect its activity. Cell-free assays can also be used to identify compounds which modulate the interaction between the polypeptide and a binding partner. In a preferred embodiment, cell-free assays for identifying such compounds consist essentially in a reaction mixture containing the polypeptide and a test compound or a library of test compounds in the presence or absence of a binding partner. A test compound can be, e.g., a derivative of a binding partner, e.g., a biologically inactive peptide, or a small molecule.

Accordingly, one exemplary screening assay of the present invention includes the steps of contacting the polypeptide or functional fragment thereof or a binding partner with a test compound or library of test compounds and detecting the formation of complexes. For detection purposes, the molecule can be labeled with a specific marker and the test compound or library of test compounds labeled with a different marker. Interaction of a test compound with a polypeptide or fragment thereof or binding partner can then be detected by determining the level of the two labels after an incubation step and a washing step. The presence of two labels after the washing step is indicative of an interaction.

An interaction between molecules can also be identified by using real-time BIA (Biomolecular Interaction Analysis, Pharmacia Biosensor AB) which detects surface plasmon resonance (SPR), an optical phenomenon. Detection depends on changes in the mass concentration of macromolecules at the biospecific interface, and does not require any labeling of interactants. In one embodiment, a library of test compounds can be immobilized on a sensor surface, e.g., which forms one wall of a micro-flow cell. A solution containing the polypeptide, functional fragment thereof, polypeptide analog or binding partner is then flown continuously over the sensor surface. A change in the

resonance angle as shown on a signal recording, indicates that an interaction has occurred. This technique is further described, e.g., in BIAtechnology Handbook by Pharmacia.

Another exemplary screening assay of the present invention includes the steps of (a) forming a reaction mixture including: (i) a polypeptide of interest, (ii) a binding partner, and (iii) a test compound; and (b) detecting interaction of the polypeptide and the binding partner. The polypeptide and binding partner can be produced recombinantly, purified from a source, e.g., plasma, or chemically synthesized, as described herein. A statistically significant change (potentiation or inhibition) in the interaction of the polypeptide and binding partner in the presence of the test compound, relative to the interaction in the absence of the test compound, indicates a potential agonist (mimetic or potentiator) or antagonist (inhibitor) of the polypeptide bioactivity for the test compound. The compounds of this assay can be contacted simultaneously. Alternatively, the polypeptide can first be contacted with a test compound for an appropriate amount of time, following which the binding partner is added to the reaction mixture. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified polypeptide or binding partner is added to a composition containing the binding partner or polypeptide, and the formation of a complex is quantified in the absence of the test compound.

Complex formation between a polypeptide and a binding partner may be detected by a variety of techniques. Modulation of the formation of complexes can be quantitated using, for example, detectably labeled proteins such as radiolabeled, fluorescently labeled, or enzymatically labeled polypeptides or binding partners, by immunoassay, or by chromatographic detection.

For processes that rely on immunodetection for quantitating one of the proteins trapped in the complex, antibodies against the protein can be used. Alternatively, the protein to be detected in the complex can be "epitope tagged" in the form of a fusion protein which includes, in addition to the polypeptide sequence, a second polypeptide for which antibodies are readily available (e.g. from commercial sources). For instance, the GST fusion proteins described above can also be used for quantification of binding using antibodies against the GST moiety. Other useful epitope tags include myc-epitopes (e.g., *see* Ellison et al. (1991) J Biol Chem 266:21150-21157) which includes a 10-residue

sequence from c-myc, as well as the pFLAG system (International Biotechnologies, Inc.) or the pEZZ-protein A system (Pharmacia, NJ).

Similar assays can be used to identify compounds that bind a protein of interest and thereby inhibit the activity of the protein.

In another embodiment, drugs are designed or optimized by monitoring the level of expression of a plurality of genes, e.g., with microarrays. In one embodiment, compounds are screened by comparing the expression level of one or more genes which are up- or down-regulated (e.g., expression profile) during bone or cartilage formation in a cell, e.g., a cell characteristic of a disease relating to bone or cartilage formation or resorption treated with a drug, relative to their expression in a reference cell, e.g., a normal cell. Optionally the expression profile is also compared to that of a cell characteristic of the disease. The comparisons are preferably done by introducing the gene expression profile data of the cell treated with the drug into a computer system comprising reference gene expression profiles which are stored in a computer readable form, using appropriate algorithms. Test compounds will be screened for those which alter the level of expression of genes, so as to bring them to a level that is similar to that in a reference or normal cell of the same type as a cell characteristic of the disease. Compounds which are capable of normalizing the expression of at least about 10%, preferably at least about 20%, 50%, 70%, 80% or 90% of the genes which are up- or down-regulated during bone or cartilage formation, are candidate therapeutics.

The efficacy of the compounds can then be tested in additional *in vitro* assays and *in vivo*, in animal models, such as the one described in the Examples. The test compound is administered to the test animal and one or more symptoms of the disease are monitored for improvement of the condition of the animal. Expression of one or more genes which are up- or down-regulated during bone or cartilage formation can also be measured before and after administration of the test compound to the animal. A normalization of the expression of one or more of these genes is indicative of the efficiency of the compound for treating a disease relating to bone or cartilage formation or resorption.

The toxicity, such as resulting from a stress-related response, of a candidate therapeutic compound can be evaluated, e.g., by determining whether it induces the expression of genes known to be associated with a toxic response. Expression of such toxicity related genes may be determined in different cell types, preferably those that are known to express the genes. In a preferred method, microarrays are used for detecting

changes in gene expression of genes known to be associated with a toxic response. Changes in gene expression may be a more sensitive marker of human toxicity than routine preclinical safety studies. It was shown, e.g., that a drug which was found not be to toxic in laboratory animals was toxic when administered to humans. When gene profiling was studied in cells contacted with the drug, however, it was found that a gene, whose expression is known to correlate to liver toxicity, was expressed (*see* below).

Such microarrays will comprise genes which are modulated in response to toxicity or stress. An exemplary array that can be used for that purpose is the Affymetrix Rat Toxicology U34 array, which contains probes of the following genes: metabolism enzymes, e.g., CYP450s, acetyltransferases, and sulfotransferases; growth factors and their receptors, e.g., IGFs, interleukins, NGTs, TGFs, and VEGT; kinases and phosphatases, e.g, lipid kinases, MAFKs, and stress-activated kinases; nuclear receptors, e.g., retinoic acid, retinoid X and PPARs; transcription factors, e.g., oncogenes, STATs, NF-kB, and zinc finger proteins; apoptosis genes, e.g., Bcl-2 genes, Bad, Bax, Caspases and Fas; stress response genes, e.g., heat-shock proteins and drug transporters; membrane proteins, e.g., gap-junction proteins and selectins; and cell-cycle regulators, e.g., cyclins and cyclin-associated proteins. Other genes included in the microarrays are only known because they contain the nucleotide sequence of an EST and because they have a connection with toxicity.

In one embodiment, a drug of interest is incubated with a cell, e.g., a cell in culture, the RNA is extracted, and expression of genes is analyzed with an array containing genes which have been shown to be up- or down-regulated in response to certain toxins. The results of the hybridization are then compared to databases containing expression levels of genes in response to certain known toxins in certain organisms. For example, the GeneLogic ToxExpress™ database can be used for that purpose. The information in this database was obtained in least in part from the use of the Affymetrix GeneChip® rat and human probe arrays with samples treated *in vivo* or *in vitro* with known toxins. The database contains levels of expression of liver genes in response to known liver toxins. These data were obtained by treating liver samples from rats treated *in vivo* with known toxins, and comparing the level of expression of numerous genes with that in rat or human primary hepatocytes treated *in vitro* with the same toxin. Data profiles can be retrieved and analyzed with the GeneExpress™ database tools, which are designed for complex data management and analysis. As indicated on the Affymetrix (Santa Clara, CA) website, the GeneLogic, Inc. (Gaithersburg, MD) has preformed proof of concept studies showing the

changes in gene expression levels can predict toxic events that were not identified by routine preclinical safety testing. GeneLogic tested a drug that had shown no evidence of liver toxicity in rats, but that later showed toxicity in humans. The hybridization results using the Affymetrix GeneChip® and GeneExpress™ tools showed that the drug caused abnormal elevations of alanine aminotransferase (ALT), which indicates liver injury, in half of the patients who had used the drug.

In one embodiment of the invention, the drug of interest is administered to an animal, such as a mouse or a rat, at different doses. As negative controls, animals are administered the vehicle alone, e.g., buffer or water. Positive controls can consist of animals treated with drugs known to be toxic. The animals can then be sacrificed at different times, e.g., at 3, 6, and 24 hours, after administration of the drug, vehicle alone or positive control drug, mRNA extracted from a sample of their liver; and the mRNA analyzed using arrays containing nucleic acids of genes which are likely to be indicative of toxicity, e.g., the Affymetrix Rat Toxicology U34 assay. The hybridization results can then be analyzed using computer programs and databases, as described above.

In addition, toxicity of a drug in a subject can be predicted based on the alleles of drug metabolizing genes that are present in a subject. Accordingly, it is known that certain enzymes, e.g., cytochrome p450 enzymes, i.e., CYP450, metabolize drugs, and thereby may render drugs which are innocuous in certain subjects, toxic in others. A commercially available array containing probes of different alleles of such drug metabolizing genes can be obtained, e.g., from Affymetrix (Santa Clara, CA), under the name of GeneChip® CYP450 assay.

Thus, a drug for a disease relating to bone or cartilage development identified as described herein can be optimized by reducing any toxicity it may have. Compounds can be derivatized *in vitro* using known chemical methods and tested for expression of toxicity related genes. The derivatized compounds must also be retested for normalization of expression levels of genes which are up- or down-regulated during bone or cartilage formation. For example, the derivatized compounds can be incubated with diseased cells of a disease relating to bone or cartilage formation or resorption, and the gene expression profile determined using microarrays. Thus, incubating cells with derivatized compounds and measuring gene expression levels with a microarray that contains the genes which are up- or down-regulated during bone or cartilage formation and a microarray containing toxicity related genes, compounds which are effective in treating diseases relating to bone

or cartilage formation or resorption and which are not toxic can be developed. Such compounds can further be tested in animal models as described above.

In another embodiment of the invention, a drug is developed by rational drug design, i.e., it is designed or identified based on information stored in computer readable form and analyzed by algorithms. More and more databases of expression profiles are currently being established, numerous ones being publicly available. By screening such databases for the description of drugs affecting the expression of at least some of the genes which are up- or down-regulated during bone or cartilage formation in a manner similar to the change in gene expression profile from a cell characteristic of a disease related to bone or cartilage formation or resorption to that of a normal counterpart cell, compounds can be identified which normalize gene expression in a cell characteristic of such a disease. Derivatives and analogues of such compounds can then be synthesized to optimize the activity of the compound, and tested and optimized as described above.

Compounds identified by the methods described above are within the scope of the invention. Compositions comprising such compounds, in particular, compositions comprising a pharmaceutically efficient amount of the drug in a pharmaceutically acceptable carrier are also provided. Certain compositions comprise one or more active compounds for treating diseases relating to bone or cartilage development.

4.4. Exemplary therapeutic compositions

Therapeutic compositions include the compounds described herein, e.g., in the context of therapeutic treatments of diseases relating to bone or cartilage formation or resorption. Therapeutic compositions may comprise one or more nucleic acids encoding a polypeptide characteristic of a disease relating to bone or cartilage formation or resorption, or equivalents thereof. The nucleic acids may be in expression vectors, e.g., viral vectors. Other compositions comprise one or more polypeptides that are up- or down-regulated during bone or cartilage formation, or equivalents thereof. Yet other compositions comprise nucleic acids encoding antisense RNA, or ribozymes, siRNAs or RNA aptamers. Also within the scope of the invention are compositions comprising compounds identified by the methods described herein. The compositions may comprise pharmaceutically acceptable excipients, and may be contained in a device for their administration, e.g., a syringe.

4.5. Administration of compounds and compositions of the invention

In a preferred embodiment, the invention provides a method for treating a subject having a disease relating to bone or cartilage formation or resorption, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising a compound of the invention.

4.5.1. Effective Dose

Compounds of the invention refer to small molecules, polypeptides, peptide mimetics, nucleic acids or any other molecule identified as potentially useful for treating diseases relating to bone or cartilage formation or resorption.

Toxicity and therapeutic efficacy of compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (The Dose Lethal To 50% Of The Population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Compounds which exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to healthy cells and, thereby, reduce side effects.

Data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

4.5.2. Formulation

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by, for example, injection, inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration. In one embodiment, the compound is administered locally, at the site where the diseased cells are present, e.g., in bone, cartilage, mesenchymal tissue, muscular tissue or in a joint.

The compounds of the invention can be formulated for a variety of loads of administration, including systemic and topical or localized administration. Techniques and formulations generally may be found in Remmington's Pharmaceutical Sciences, Meade Publishing Co., Easton, PA. For systemic administration, injection is preferred, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the compounds of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets, lozanges, or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., ationd oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts,

flavoring, coloring and sweetening agents as appropriate. Preparations for oral administration may be suitably formulated to give controlled release of the active compound.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Administration, e.g., systemic administration, can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For

topical administration, the compounds of the invention can be formulated into ointments, salves, gels, or creams as generally known in the art. A wash solution can be used locally to treat an injury or inflammation to accelerate healing.

In clinical settings, a gene delivery system for a gene of interest can be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g., by intravenous injection, and specific transduction of the protein in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the subject or animal being quite localized. For example, the gene delivery vehicle can be introduced by catheter (*see* U.S. Patent 5,328,470) or by stereotactic injection (e.g., Chen et al. (1994) PNAS 91: 3054-3057). A nucleic acid, such as one encoding a polypeptide of interest or homologue thereof can be delivered in a gene therapy construct by electroporation using techniques described, for example, by Dev et al. ((1994) Cancer Treat Rev 20:105-115). Gene therapy can be conducted *in vivo* or *ex vivo*.

The pharmaceutical preparation of the gene therapy construct or compound of the invention can consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle or compound is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

The therapeutic method may include administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage, tissue damage or diseased cells. Topical administration may be suitable for wound healing and tissue repair. Therapeutically

useful agents other than the gene-specific therapeutics which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with a composition of the invention. The compositions of the invention may be employed in association with surgery. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the therapeutics to the site of bone and/or cartilage damage or other target site, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material may be based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions of the invention will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

The dosage regimen will be determined by the attending physician considering various factors which modify the action of the therapeutics, e.g. amount of bone weight desired to be formed, the site of bone damage or diseased cells, the condition of the damaged bone, the type of disease, the size of a wound, type of damaged tissue, the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and the types of therapeutics in the composition. The addition of other known growth factors, such as BMP-2 and IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of bone growth and/or repair, for example, x-rays, histomorphometric determinations and tetracycline labeling.

5. Exemplary kits

The invention further provides kits for determining the expression level of genes which are up- or down-regulated during bone or cartilage formation or resorption. The kits may be useful for identifying subjects that are predisposed to developing or who have a disease relating to bone or cartilage formation or resorption, as well as for identifying and validating therapeutics for such diseases. In one embodiment, the kit comprises a computer readable medium on which is stored one or more gene expression profiles, e.g., of mesenchymal cells differentiating into bone or cartilage cells, or of diseased cells of a disease relating to bone or cartilage formation or resorption, or at least values representing levels of expression of one or more genes which are up- or down-regulated during bone or cartilage formation. The computer readable medium can also comprise gene expression profiles of counterpart normal cells, such as the expression profiles set forth in Tables 1, 2, 5 and/or 6; diseased cells treated with a drug, and any other gene expression profile described herein. The kit can comprise expression profile analysis software capable of being loaded into the memory of a computer system.

A kit can comprise a microarray comprising probes of genes which are up- or down-regulated during bone or cartilage formation. A kit can comprise one or more probes or primers for detecting the expression level of one or more genes which are up- or down-regulated during bone or cartilage formation and/or a solid support on which probes are attached and which can be used for detecting expression of one or more genes which are up- or down-regulated during bone or cartilage formation in a sample. A kit may further comprise nucleic acid controls, buffers, and instructions for use.

Other kits provide compositions for treating a disease relating to bone or cartilage formation or resorption. For example, a kit may comprise one or more nucleic acids corresponding to one or more genes which are up- or down-regulated during bone or cartilage formation, e.g., for use in treating a patient having a disease relating to bone or cartilage formation or resorption. The nucleic acids can be included in a plasmid or a vector, e.g., a viral vector. Other kits comprise a polypeptide encoded by a gene that is up- or down-regulated during bone or cartilage formation or an antibody to a polypeptide. Yet other kits comprise compounds identified herein as agonists or antagonists of genes which are up- or down-regulated during bone or cartilage formation. The compositions may be pharmaceutical compositions comprising a pharmaceutically acceptable excipient.

Yet other kits comprise components for the identification of drugs that modulate the activity of a protein encoded by a gene that is up- or down-regulated during bone or cartilage formation. Exemplary kits may comprise a polypeptide encoded by a gene or a nucleic acid encoding such a polypeptide that is listed in any of the Tables described herein.

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references including literature references, issued patents, published and non published patent applications as cited throughout this application are hereby expressly incorporated by reference.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. (*See*, for example, *Molecular Cloning A Laboratory Manual, 2nd Ed.*, ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); Oligonucleotide Synthesis (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No: 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); (R. I. Freshney, Alan R. Liss; Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); , Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986) (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

Examples

Example 1

This Example describes the identification of genes which are up- and down-regulated during hBMP-2 induced ectopic bone formation in mouse quadriceps muscles

The following animal model of ectopic bone formation was used. Human BMP-2 (Wyeth Research Division of Wyeth Pharmaceuticals, Inc.) was diluted to a final concentration of 1 mg/ml in formulation buffer (0.5% sucrose, 2.5% glycine, 5 mM L-glutamic acid, 5 mM NaCl, 0.01% polysorbate 80, pH 4.5) (Wyeth Research Division of Wyeth Pharmaceuticals, Inc., MFR00842). Female B6.CB17-Prkdc<SCID>SzJ mice (~ 14 weeks of age; Jackson Lab.) were randomly assigned to either a control or an experimental group. Mice in the control group were injected with 50 µl of formulation buffer into the quadriceps muscle of each leg. Similarly, mice in the experimental group were injected with 50 µg of recombinant human BMP-2 (hBMP-2) in formulation buffer. Care was taken to ensure that each injection was made into the middle of the muscle mass. In both groups, three mice were used for each time point. Mice were euthanized on days 1, 2, 3, 4, 7 and 14. The entire quadriceps muscle was removed from each leg and muscles selected for RNA analysis were snap frozen in liquid nitrogen and stored at –80 degrees Celsius. Total RNA was prepared for each sample. Equal amounts of RNA from the three control samples were pooled to create a single control sample for each time point.

GeneChip (Affymetrix, San Jose, CA) hybridization solutions were prepared as described previously (Lockhart, D.J., et al. (1996) Nature Biotechnol. 14:1675-1680 and Wilson, S.B., et al. (2000) Proc. Nat. Acad Sci. USA 97:7411-7416). Murine Genome U74 chips (Affymetrix cat. # 900322, 900324, 900326) were scanned with the use of protocols recommended by Affymetrix and data was collected/reduced with the use of the GeneChip 3.1 application (Affymetrix). To identify differentially expressed genes, GeneChip 3.1 was used to make three separate, time-matched, comparisons between a "pooled" buffer (control) and three hBMP-2 (experimental) samples.

Changes in gene expression, for each day of the experiment, were compiled into an Excel table. This table contained only those genes that satisfied the following two criteria for at least one time point of the experiment: i) the gene was Present in either or both the control and experimental samples; and ii) relative to the control sample, gene expression in the experimental sample was called Increasing or Decreasing. This composite table was

imported into GeneSpring 3.2.12 (Silicon Genetics) for graphical analysis and for the creation of the expression profile gene lists. Table 1 lists genes on the U74 arrays that show at least a two-fold increase in gene expression on at least one day of the experiment. Table 2 lists genes on the U74 arrays that show at least a two-fold decrease in gene expression on at least one day of the experiment.

An expression analysis using the RNA obtained as described above was also conducted on another set of gene microarrays (Wyeth Research Division of Wyeth Pharmaceuticals, Inc.). Genes which were found to be up- or down-regulated by a factor of at least about 4 are set forth in Tables 5 and 6. The numbers represent fold change (Gene Frequency$_{BMP-2}$/Gene Frequency$_{Buffer}$) in gene expression + the standard deviation (n=3). The genes listed in Table 7 and many others listed in Tables 1 and 2 do not appear to have been associated with bone or cartilage formation before.

Example 2: MMP23 and CLF-1 are up-regulated during bone and cartilage formation

Two genes which have not previously been known to be associated with bone or cartilage development appear to be up-regulated at very high levels. The first gene is Cytokine Receptor-like Factor 1 (CLF-1) and the second gene is Matrix MetalloProtease 23 (MMP23). Graphs representing the change in gene expression of each of these genes over time during bone formation in the above-described animal model are set forth in Figures 1 and 2. These graphs show that CLF-1 is maximally up-regulated about 15 fold and MMP23 is maximally up-regulated about 40 fold.

To identify cells that express MMP23 and CLF-1, in situ hybridization was performed on tissue sections from mucles of mice injected or not with recombinant hBMP-2. No signal was detected with a sense or antisense probe directed against the message for CLF-1 in any cell type or at any time point in sections from muscles injected with buffer only. In contrast, the anti-sense probe was detected in sections from muscle injected with hBMP-2. Staining was detected at all time points in this treatment group, and these results are summarized in Table 4. In particular, staining was observed in hypertrophic chondrocytes on day 7 and osteoblasts and some marrow cells on day 14.

No signal was detected with a sense or antisense probe directed against the message for MMP23 in any cell type or at any time point in sections from muscles injected with buffer only. In contrast, the anti-sense probe detected MMP23 mRNA in sections from muscles injected with hBMP-2. Staining was detected at all time points in this treatment group, and these results are summarized in Table 5. Staining was observed in hypertrophic chondrocytes and osteblasts on days 7 and 14, respectively.

Table 4. Summary of cells stained with an antisense probe for CLF-1 mRNA*

		Day					
Treatment	CLF-1 mRNA Positive Cell	1	2	3	4	7	14
BUFFER	Fibroblast	–	–	–	–	–	–
	Macrophage	–	–	–	–	–	–
	Chondrocyte-like	N/A	N/A	N/A	N/A	N/A	N/A
	Chondrocyte	N/A	N/A	N/A	N/A	N/A	N/A
	Marrow cell	N/A	N/A	N/A	N/A	N/A	N/A
	Osteoblast/Osteocyte	N/A	N/A	N/A	N/A	N/A	N/A
HBMP-2	Fibroblast	+	++	++	++	-	-
	Macrophage	++	+	++	++	-	-
	Chondrocyte-like	N/A	N/A	N/A	++	N/A	N/A
	Chondrocyte	N/A	N/A	N/A	N/A	+	N/A
	Marrow cell	N/A	N/A	N/A	N/A	N/A	+
	Osteoblast/Osteocyte	N/A	N/A	N/A	N/A	N/A	+

* Binding of sense probe was not detected in either treatment group.

N/A: Cell type not present in section.
+: Slight staining intensity
++: Mild staining intensity
-: Staining not detected

Table 1 Treatment Time	BMP2 day 01	BMP2 day 02	BMP2 day 03	BMP2 day 04	BMP2 day 07	BMP2 day 14		
Affymetrix Qualifier	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Gene Name	Genbank Accession #
110451_at	2.76	4.33	4.35	2.49	0.00	3.90	UNK_AI646968	AI646968
92315_at	2.86	0.00	6.24	8.35	0.00	3.87	SLFN4	AF099977
93285_at	0.00	2.14	2.31	2.81	0.00	2.94	UNK_AI845584	AI845584
103563_at	0.00	4.54	5.11	2.68	0.00	5.42	UNK_AW125713	AW125713
107566_at	0.00	1.55	3.55	3.44	2.08	17.15	UNK_AI849532	AI849532
115395_at	0.00	2.23	3.68	2.97	0.00	2.37	UNK_AW208422	AW208422
92718_at	0.00	1.68	2.17	3.31	0.00	2.34	UNK_AI158810	AI158810
93975_at	0.00	1.77	2.83	3.21	0.00	3.81	33 POLYPEPTIDE [R.NORVEGICUS]	AI853531
96752_at	1.65	2.58	0.00	3.13	0.00	2.46	ICAM1	M90551
103446_at	0.00	0.00	3.81	5.48	0.00	3.13	UNK_AA959954	AA959954
104177_at	0.00	0.00	3.59	2.98	0.00	2.50	UNK_AA204579	AA204579
104252_at	0.00	0.00	2.17	2.34	0.00	2.47	UNK_AW123823	AW123823
108877_at	0.00	0.00	2.69	2.18	0.00	2.40	UNK_AI790579	AI790579
109102_r_at	0.00	1.67	2.79	2.38	0.00	2.61	UNK_AI838972	AI838972
109922_at	0.00	3.60	0.00	4.21	0.00	3.09	UNK_AW122872	AW122872
112478_at	0.00	0.00	2.02	2.33	0.00	2.33	UNK_AI853409	AI853409
112671_at	0.00	0.00	2.84	5.17	0.00	3.73	UNK_AW122101	AW122101
113758_at	0.00	0.00	0.00	3.78	3.50	23.28	UNK_AI843230	AI843230
115573_at	0.00	4.17	3.10	0.00	0.00	2.99	UNK_AW047581	AW047581
130459_at	0.00	2.06	3.92	4.75	-1.78	0.00	UNK_AI845691	AI845691
136655_f_at	0.00	0.00	2.87	3.14	0.00	2.39	UNK_AI841502	AI841502
94354_at	0.00	0.00	0.00	2.22	0.00	3.75	UNK_AI845514	AI845514
95303_at	1.49	2.01	0.00	0.00	0.00	2.63	0	AA144469
96481_at	***0.00***	***0.00***	***0.00***	***0.00***	***2.83***	***36.90***	***UNK_AV251613***	***AV251613***
97448_at	0.00	0.00	0.00	2.66	0.00	2.62	UNK_AI845165	AI845165
100880_at	0.00	0.00	0.00	2.42	0.00	4.34	UNK_AA816121	AA816121
101327_at	0.00	0.00	0.00	2.17	0.00	4.31	UNK_U82610	U82610
103672_at	0.00	0.00	0.00	2.19	0.00	2.02	UNK_AW122572	AW122572
104193_at	0.00	0.00	0.00	2.01	0.00	2.39	UNK_AW047583	AW047583
104195_at	0.00	1.87	0.00	3.08	0.00	2.77	UNK_AA939440	AA939440
106500_f_at	0.00	0.00	0.00	2.13	0.00	2.86	UNK_AI642841	AI642841
106583_at	0.00	1.46	0.00	2.34	0.00	2.21	UNK_AI851530	AI851530
106644_at	0.00	0.00	0.00	2.64	0.00	6.71	UNK_AW047110	AW047110
106957_f_at	0.00	0.00	2.15	0.00	0.00	3.34	UNK_AI790368	AI790368
108494_at	0.00	0.00	0.00	2.39	0.00	3.23	UNK_AW123118	AW123118
109099_at	0.00	0.00	2.31	0.00	0.00	2.30	UNK_AW049860	AW049860
109345_at	1.60	2.28	2.23	1.95	0.00	1.75	UNK_AA711635	AA711635
112015_at	0.00	0.00	0.00	2.37	0.00	5.77	UNK_AI551067	AI551067
112908_at	0.00	0.00	0.00	2.18	0.00	2.63	UNK_AI849021	AI849021
113181_r_at	0.00	0.00	0.00	2.41	0.00	3.28	UNK_AW125085	AW125085
113248_at	0.00	1.70	2.32	0.00	0.00	3.11	UNK_AI837648	AI837648
113724_at	0.00	0.48	2.16	1.55	1.17	7.05	UNK_AI848964	AI848964
113865_at	0.00	0.00	0.00	2.39	0.00	2.52	UNK_AA231562	AA231562
114306_at	0.00	0.00	2.13	0.00	0.00	2.92	UNK_AI593556	AI593556
114380_at	0.00	1.57	0.00	2.43	0.00	3.41	UNK_AA959464	AA959464
115397_at	0.00	0.00	0.00	3.18	0.00	4.45	UNK_AA727857	AA727857
115453_at	0.00	0.00	0.00	0.00	2.04	23.84	UNK_AA764584	AA764584
115520_at	0.00	0.00	0.00	2.91	0.00	3.20	UNK_AA163981	AA163981
115874_at	0.00	0.00	0.00	2.93	0.00	3.18	UNK_AW046286	AW046286
116418_at	0.00	0.00	0.00	3.54	0.00	5.07	UNK_AA839780	AA839780
117265_at	0.00	0.00	2.93	0.00	0.00	4.66	UNK_AI853644	AI853644
134205_at	0.00	0.00	0.00	2.79	0.00	2.04	UNK_AI482096	AI482096

134405_at	0.00	0.00	0.00	2.03	0.00	3.36	UNK_AI662230	AI662230
138037_at	0.00	0.00	0.00	2.32	0.00	2.43	UNK_AI851460	AI851460
92378_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.69***	***UNK_AI849305***	***AI849305***
92474_at	0.00	0.00	0.00	0.00	0.00	2.13	UNK_AF083497	AF083497
93153_at	0.00	0.00	0.00	0.00	0.40	2.46	UNK_AW124433	AW124433
93475_at	0.00	0.00	0.00	0.00	0.00	2.60	UNK_AI845581	AI845581
93482_at	0.00	0.00	0.00	0.00	0.00	2.28	UNK_AI117835	AI117835
93647_at	0.00	0.00	0.00	0.00	0.00	3.25	UNK_AI152195	AI152195
93837_at	0.00	0.00	0.00	0.00	0.00	3.92	UNK_AI786089	AI786089
94347_i_at	0.00	0.00	0.00	0.00	0.00	2.23	UNK_AW124044	AW124044
94352_at	0.00	0.00	0.00	0.00	0.00	2.50	UNK_AI850675	AI850675
94362_at	0.00	1.77	0.00	2.00	0.00	1.81	UNK_AI843682	AI843682
94364_at	0.00	0.00	0.00	0.00	0.00	2.74	UNK_AI847926	AI847926
94460_at	0.00	0.00	0.00	1.78	0.00	2.16	UNK_AA691445	AA691445
94471_r_at	0.00	0.00	0.00	0.00	0.00	2.86	UNK_AW045974	AW045974
94512_f_at	0.00	0.00	0.00	1.95	0.00	2.91	UNK_AI843210	AI843210
95165_at	0.00	0.00	0.00	0.00	0.00	3.48	0	AA409156
95620_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.11***	***UNK_AW120882***	***AW120882***
95914_at	0.00	0.00	0.00	0.00	0.00	2.09	UNK_AA177382	AA177382
96165_at	0.00	0.00	0.00	0.00	0.00	2.08	UNK_AW125109	AW125109
96172_at	0.00	0.00	0.00	0.00	0.00	3.73	UNK_AA795946	AA795946
96187_at	0.00	0.00	0.00	0.00	0.00	2.40	UNK_AI837021	AI837021
96785_at	0.00	0.00	0.00	0.00	0.00	2.14	UNK_AF110520	AF110520
96790_f_at	0.00	0.00	0.00	0.00	0.00	2.16	UNK_AW125222	AW125222
96806_at	0.00	0.00	0.00	0.00	0.00	2.70	UNK_AI843802	AI843802
96862_at	0.00	0.00	0.00	1.98	0.00	2.03	UNK_AI848584	AI848584
96881_at	0.00	0.00	0.00	1.79	0.00	2.31	UNK_AW049394	AW049394
97131_at	0.00	0.00	0.00	0.00	0.00	2.66	UNK_AW124615	AW124615
97197_r_at	0.00	0.00	0.00	2.21	0.00	1.78	UNK_C78850	C78850
97386_at	0.00	0.00	0.00	0.00	0.00	2.29	UNK_AI853294	AI853294
97598_at	0.00	0.00	0.00	0.00	0.00	3.27	UNK_AW209139	AW209139
97864_at	0.00	0.00	0.00	0.00	0.00	2.90	UNK_AW258842	AW258842
97866_at	0.00	0.00	0.00	0.00	0.00	2.12	UNK_AI842858	AI842858
97944_f_at	0.00	0.00	0.00	0.00	0.00	3.30	UNK_AF099808	AF099808
97967_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.08***	***UNK_AA881438***	***AA881438***
98104_at	0.00	0.00	0.00	0.00	0.00	2.65	UNK_AI842889	AI842889
98154_at	0.00	0.00	0.00	2.56	0.00	1.79	UNK_AW050133	AW050133
98572_at	0.00	0.00	1.76	2.55	0.00	1.86	UNK_AW122551	AW122551
98849_at	0.00	0.00	0.00	0.00	0.00	2.52	UNK_AI463656	AI463656
98908_at	0.00	0.00	0.00	1.67	0.00	2.04	UNK_AW125510	AW125510
98988_at	0.00	0.00	0.00	2.11	0.00	1.77	0	AA614971
99178_at	0.00	0.00	0.00	0.00	0.00	2.09	UNK_AI845652	AI845652
99379_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.39***	***0***	***M27034***
99592_f_at	0.00	0.00	0.00	0.00	0.00	2.16	UNK_AB030505	AB030505
100297_at	0.00	0.00	0.00	0.00	0.00	2.38	UNK_AA693125	AA693125
100890_at	0.00	0.00	0.00	0.00	0.00	2.48	UNK_AI173038	AI173038
101221_at	0.00	1.67	1.61	2.10	0.00	1.90	0	C76746
102009_at	0.00	0.00	0.00	0.00	0.00	3.95	UNK_AI835274	AI835274
102348_at	0.00	0.00	0.00	1.85	0.00	2.42	XDH	AI551087
102383_at	0.00	0.00	0.00	0.00	0.00	3.66	UNK_AW048977	AW048977
102863_at	0.00	0.00	0.00	0.00	0.00	2.16	UNK_AI550530	AI550530
103356_at	0.00	0.00	0.00	0.00	0.00	2.97	UNK_AI843267	AI843267
103424_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.23***	***UNK_AI844839***	***AI844839***
103451_at	0.00	0.00	0.00	0.00	0.00	2.30	UNK_AI835159	AI835159
103493_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***7.57***	***UNK_AW045989***	***AW045989***
103582_r_at	0.00	0.00	0.00	0.00	0.00	2.59	UNK_AI845633	AI845633
103678_at	0.00	0.00	0.00	0.00	0.00	2.22	UNK_AI841139	AI841139
103697_at	0.00	0.00	0.00	0.00	0.00	3.81	UNK_AW061234	AW061234
103901_at	0.00	0.00	0.00	0.00	0.00	2.52	UNK_AW213777	AW213777

103923_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***13.09***	***UNK_AA656014***	***AA656014***
103957_at	0.00	0.00	0.00	0.00	-2.38	2.04	Trfr	X57349
104036_at	0.00	0.00	0.00	0.00	0.00	2.39	UNK_AI845447	AI845447
104058_at	0.00	0.00	0.00	1.82	0.00	2.49	UNK_AW047528	AW047528
104118_at	0.00	0.00	0.00	0.00	0.00	2.29	UNK_AW123781	AW123781
104150_at	0.00	2.31	0.00	0.00	0.00	1.72	UNK_AW121957	AW121957
104274_at	0.00	0.00	0.00	0.00	0.00	2.47	UNK_AW124843	AW124843
104316_at	0.00	0.00	0.00	0.00	0.00	2.69	UNK_AI646098	AI646098
104326_at	0.00	0.00	0.04	0.00	0.00	2.48	UNK_AI838951	AI838951
104477_at	0.00	0.00	0.00	0.00	0.00	3.25	UNK_AW047643	AW047643
104494_at	0.00	0.00	0.00	0.00	0.00	2.16	UNK_AI642098	AI642098
104513_at	0.00	0.00	0.00	0.00	0.00	2.22	EST; unknown	AA688938
104550_at	0.00	0.00	0.00	0.00	0.00	2.32	UNK_AW123273	AW123273
105005_at	0.00	0.00	0.00	0.00	0.00	2.02	UNK_AI020518	AI020518
105143_at	0.00	0.00	0.00	0.00	0.00	2.81	UNK_AI852801	AI852801
105159_at	0.00	0.00	0.00	0.00	0.00	2.62	UNK_AI843003	AI843003
105317_at	0.00	0.00	0.00	0.00	0.00	2.61	UNK_AI876413	AI876413
105455_at	0.00	0.00	0.00	0.00	0.00	2.53	UNK_AI606142	AI606142
105554_at	0.00	0.00	0.00	0.00	0.00	2.08	UNK_AA177721	AA177721
105574_i_at	0.00	0.00	0.00	2.19	0.00	1.96	UNK_AA833192	AA833192
105686_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.01***	***UNK_AI836126***	***AI836126***
105689_r_at	0.00	0.00	0.00	0.00	0.00	2.68	UNK_AI842855	AI842855
106101_at	0.00	0.00	0.00	1.63	0.00	2.91	UNK_AI853221	AI853221
106184_at	0.00	0.00	0.00	0.00	0.00	2.88	UNK_AI848994	AI848994
106189_at	0.00	0.00	0.00	0.00	0.00	2.53	UNK_AI225382	AI225382
106262_at	0.00	0.00	0.00	0.00	0.00	2.08	UNK_AA914186	AA914186
106479_at	0.00	0.00	0.00	0.00	0.00	2.53	UNK_AI844057	AI844057
106491_at	0.00	0.00	0.00	0.00	0.00	2.06	UNK_AI957035	AI957035
106536_f_at	0.00	0.00	0.00	0.00	0.00	2.86	UNK_AI786456	AI786456
106616_at	0.00	0.00	0.00	0.00	0.00	2.12	UNK_AA139123	AA139123
106617_at	0.00	0.00	0.00	0.00	0.00	2.16	UNK_AW123240	AW123240
106635_at	0.00	0.00	0.00	0.00	0.00	3.61	UNK_AA764553	AA764553
106637_r_at	0.00	0.00	0.00	0.00	0.00	2.79	UNK_AI647933	AI647933
106648_at	0.00	0.00	0.00	0.00	0.00	2.85	UNK_AW045837	AW045837
106654_at	0.00	0.00	0.00	0.00	0.00	2.82	UNK_AA647503	AA647503
106868_at	0.00	0.00	0.00	0.00	0.00	2.33	UNK_AW048984	AW048984
106958_r_at	0.00	0.00	0.00	0.00	0.00	3.40	UNK_AI790368	AI790368
107045_at	0.00	1.82	0.00	0.00	0.00	2.29	UNK_AA840458	AA840458
107064_at	0.00	0.00	1.47	0.00	0.00	2.10	UNK_AA645686	AA645686
107273_at	0.00	0.00	0.00	0.00	0.00	2.03	UNK_AW046853	AW046853
107459_at	0.00	0.00	0.00	0.00	0.00	3.47	UNK_AW049987	AW049987
107483_at	0.00	0.00	0.00	0.00	0.00	2.14	UNK_AW050172	AW050172
107552_at	0.00	0.00	0.00	0.00	0.00	2.74	UNK_AA711627	AA711627
107602_at	0.00	0.00	0.00	0.00	0.00	3.00	UNK_AA717340	AA717340
107609_at	0.00	0.00	0.00	0.00	0.00	3.22	UNK_AA137485	AA137485
107766_at	0.00	0.00	0.00	0.00	0.00	2.74	UNK_AI426461	AI426461
107787_at	0.00	0.00	0.00	0.00	0.00	2.22	UNK_AA755149	AA755149
107871_at	0.00	1.46	0.00	0.00	0.00	2.69	UNK_AW048252	AW048252
107995_at	0.00	0.00	0.00	0.00	0.00	2.14	UNK_AI845884	AI845884
108073_at	0.00	0.00	0.00	0.00	0.00	2.92	UNK_AI850676	AI850676
108312_at	0.00	0.00	0.00	0.00	0.00	2.66	UNK_AI593736	AI593736
108329_at	0.00	0.00	0.00	0.00	0.00	2.46	UNK_AA833472	AA833472
108352_at	0.00	0.00	0.00	0.00	0.00	2.32	UNK_AW061021	AW061021
108368_at	0.00	0.00	0.00	0.00	0.00	2.08	UNK_AI121297	AI121297
108375_at	0.00	0.00	0.00	0.00	0.00	2.22	UNK_AA982346	AA982346
108492_at	0.00	0.00	0.00	1.05	0.00	4.22	UNK_AI852003	AI852003
108519_at	0.00	0.00	0.00	0.00	0.00	2.72	UNK_AW212926	AW212926
108556_at	0.00	0.00	0.00	0.00	0.00	2.50	UNK_AI851581	AI851581
108733_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***19.06***	***UNK_AW120982***	***AW120982***

109066_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.85***	***UNK_AA874293***	***AA874293***
109081_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.41***	***UNK_AI119897***	***AI119897***
109092_at	0.00	0.00	0.00	0.00	0.00	2.32	UNK_AA763190	AA763190
109176_at	0.00	0.00	0.00	0.00	0.00	2.47	UNK_AI846059	AI846059
109326_at	0.00	0.00	0.00	0.00	0.00	2.72	UNK_AI837923	AI837923
109410_at	0.00	0.00	0.00	0.00	0.00	2.67	UNK_AW121121	AW121121
109453_at	0.00	0.00	0.00	0.00	0.00	2.98	UNK_AW044905	AW044905
109561_at	0.00	0.00	0.00	1.77	0.00	2.55	UNK_AA032690	AA032690
109729_at	0.00	0.00	0.00	0.00	0.00	3.09	UNK_AI226312	AI226312
109747_at	0.00	0.00	0.00	0.00	0.00	2.66	UNK_AW046149	AW046149
109758_at	0.00	0.00	0.00	0.00	0.00	2.07	UNK_AW124910	AW124910
109785_at	0.00	0.00	0.00	0.00	0.00	2.45	UNK_AW123736	AW123736
109807_f_at	0.00	0.00	0.00	0.00	0.00	2.28	TSGA12	AI117666
109813_f_at	0.00	0.00	0.00	0.00	0.00	2.10	UNK_AI413781	AI413781
109923_at	0.00	0.00	0.00	1.67	0.00	2.09	UNK_AA792733	AA792733
109945_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.10***	***UNK_AI850918***	***AI850918***
109962_at	0.00	0.00	0.00	0.00	0.00	3.36	UNK_AI314322	AI314322
109970_at	0.00	0.00	0.00	0.00	0.00	2.61	UNK_AI843938	AI843938
110168_at	0.00	0.00	0.00	0.00	0.00	3.15	UNK_AW124258	AW124258
110331_at	0.00	0.00	0.00	0.00	0.00	3.16	UNK_AI851383	AI851383
110355_at	0.00	0.00	0.00	0.00	0.00	2.86	UNK_AW049880	AW049880
110374_at	0.00	0.00	0.00	0.00	0.00	2.98	UNK_AI851558	AI851558
110396_at	0.00	0.00	0.00	0.00	0.00	2.93	UNK_AW050339	AW050339
110472_f_at	0.00	0.00	0.00	0.00	0.00	2.23	UNK_AW121052	AW121052
110515_at	0.00	0.00	0.00	1.94	0.00	2.61	UNK_AW123207	AW123207
110570_at	0.00	0.00	0.00	0.00	0.00	2.39	UNK_AA118312	AA118312
110616_at	0.00	0.00	0.00	0.00	0.00	2.28	UNK_AI646542	AI646542
110712_at	0.00	0.00	0.00	0.00	0.00	2.14	UNK_AA863810	AA863810
110758_at	0.00	0.00	0.00	0.00	0.00	2.61	UNK_AA915391	AA915391
110790_at	0.00	-1.32	0.00	0.00	0.00	3.19	UNK_AW121879	AW121879
110833_at	0.00	0.00	0.00	0.00	0.00	2.59	UNK_AI847626	AI847626
110834_at	0.00	0.00	0.00	0.00	0.00	3.53	UNK_AA919801	AA919801
110839_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.31***	***UNK_AI839647***	***AI839647***
110852_at	0.00	0.00	0.00	1.38	0.00	2.51	UNK_AI226234	AI226234
111036_f_at	0.00	0.00	0.00	0.00	0.00	3.48	UNK_AI882445	AI882445
111083_at	0.00	0.00	0.00	0.00	0.00	3.25	UNK_AW122341	AW122341
111191_at	0.00	0.00	0.00	0.00	0.00	3.55	UNK_AW120521	AW120521
111233_at	0.00	0.00	0.00	0.00	0.00	3.31	UNK_AW122352	AW122352
111309_at	0.00	0.00	0.00	0.00	0.00	2.88	UNK_AI181332	AI181332
111405_at	0.00	0.00	0.00	0.00	0.00	2.17	UNK_AI847396	AI847396
111439_at	0.00	0.00	0.00	0.00	0.00	2.69	UNK_AI591562	AI591562
111515_at	0.00	0.00	0.00	0.00	0.00	3.71	UNK_AW060320	AW060320
111682_at	0.00	0.00	0.00	0.00	0.00	2.47	UNK_AW229627	AW229627
111707_at	0.00	0.00	0.00	0.00	0.00	2.37	UNK_AW259521	AW259521
111738_at	0.00	0.00	0.00	0.00	0.00	2.54	UNK_AW121627	AW121627
111790_at	0.00	0.00	0.00	0.00	0.00	2.80	UNK_AW122322	AW122322
111916_at	0.00	0.00	0.00	0.00	0.00	2.06	UNK_AI841396	AI841396
111924_at	0.00	0.00	0.00	0.00	0.00	2.33	UNK_AA789586	AA789586
112020_g_at	0.00	0.00	0.00	0.00	0.00	3.63	UNK_AA881092	AA881092
112084_at	0.00	0.00	0.00	1.49	0.00	2.11	UNK_AI662678	AI662678
112351_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.17***	***UNK_AW048346***	***AW048346***
112388_at	0.00	0.00	0.00	0.00	0.00	2.20	UNK_AW123069	AW123069
112435_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.03***	***UNK_AW061103***	***AW061103***
112802_at	0.00	0.00	0.00	0.00	0.00	2.65	UNK_AW122077	AW122077
112858_at	0.00	0.00	0.00	0.00	0.00	2.94	UNK_AI854616	AI854616
112918_at	0.00	0.00	0.00	0.00	0.00	3.95	UNK_AI842563	AI842563
112944_at	0.00	0.00	0.00	1.46	0.00	2.25	UNK_AI607994	AI607994
112949_at	0.00	0.00	0.00	0.00	0.00	2.74	UNK_AA915460	AA915460
113019_at	0.00	0.00	0.00	0.00	0.00	2.62	UNK_AA138087	AA138087

113020_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.44***	***UNK_AA967744***	***AA967744***
113044_at	0.00	0.00	0.00	0.00	0.00	3.47	UNK_AA002573	AA002573
113130_at	0.00	0.00	0.00	0.00	0.00	2.36	UNK_AI854014	AI854014
113131_at	0.00	0.00	0.00	0.00	0.00	2.71	UNK_AW047592	AW047592
113171_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.72***	***UNK_AI849023***	***AI849023***
113227_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***6.08***	***UNK_AI854880***	***AI854880***
113240_at	0.00	0.00	0.00	1.73	0.00	2.76	UNK_AA153179	AA153179
113246_at	0.00	0.00	0.00	0.00	0.00	2.29	UNK_AI156068	AI156068
113287_at	0.00	0.00	0.00	0.00	0.00	3.02	UNK_AI115322	AI115322
113311_r_at	0.00	0.00	0.00	0.00	0.00	2.64	UNK_AA175228	AA175228
113316_at	0.00	0.00	0.00	0.00	0.00	3.21	UNK_AI841062	AI841062
113319_at	0.00	0.00	0.00	0.00	0.00	3.04	UNK_AI786159	AI786159
113339_at	0.00	0.00	0.00	0.00	0.00	2.24	UNK_AW046072	AW046072
113554_at	0.00	0.00	0.00	0.00	0.00	2.53	UNK_AI840943	AI840943
113579_at	0.00	0.00	0.00	0.00	0.00	2.33	UNK_AI842229	AI842229
113680_at	0.00	0.00	0.00	1.91	0.00	2.52	UNK_AI846297	AI846297
113737_at	0.00	0.00	0.00	0.00	0.00	2.30	UNK_AW122351	AW122351
113790_at	0.00	0.00	0.00	1.63	0.00	3.67	UNK_AI194566	AI194566
114005_at	0.00	0.00	0.00	1.75	0.00	3.24	UNK_AW215403	AW215403
114016_at	0.00	0.00	0.00	0.00	0.00	2.30	UNK_AW124568	AW124568
114045_at	0.00	0.00	0.00	0.00	0.00	2.70	UNK_AI877454	AI877454
114149_at	0.00	0.00	0.00	0.00	0.00	2.05	UNK_AA596704	AA596704
114197_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.89***	***UNK_AI643902***	***AI643902***
114213_at	0.00	0.00	0.00	0.00	0.00	2.45	UNK_AA242681	AA242681
114270_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***12.52***	***UNK_AW049906***	***AW049906***
114281_at	0.00	0.00	0.00	1.98	0.00	5.21	UNK_AI593204	AI593204
114309_at	0.00	0.00	0.00	0.00	0.00	2.11	UNK_AA716898	AA716898
114390_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.05***	***UNK_AI464339***	***AI464339***
114408_at	0.00	0.00	0.00	0.00	0.00	2.77	UNK_AI843543	AI843543
114463_at	0.00	0.00	0.00	0.00	0.00	2.40	UNK_AI585881	AI585881
114485_at	0.00	0.00	0.00	1.71	0.00	2.72	UNK_AI596717	AI596717
114619_at	0.00	0.00	0.00	1.83	0.00	2.26	UNK_AA797871	AA797871
114686_at	0.00	0.00	0.00	0.00	0.00	2.30	UNK_AW048693	AW048693
114716_at	0.00	0.00	0.00	0.00	0.00	2.26	UNK_AI181770	AI181770
114752_at	0.00	-2.01	0.00	0.00	0.00	2.84	UNK_AI843572	AI843572
114755_at	0.00	0.00	0.00	0.00	0.00	2.34	UNK_AI844350	AI844350
114804_at	0.00	0.00	0.00	0.00	0.00	2.22	NNAT	AI154029
114836_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.17***	***UNK_AI536480***	***AI536480***
114854_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.39***	***UNK_AI843070***	***AI843070***
114917_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.31***	***UNK_AI118679***	***AI118679***
114980_at	0.00	0.00	0.00	0.00	0.00	2.28	UNK_AI854024	AI854024
115004_at	0.00	0.00	0.00	0.00	0.00	2.23	UNK_AI788664	AI788664
115017_at	0.00	0.00	0.00	1.79	0.00	2.11	UNK_AI848298	AI848298
115058_at	0.00	0.00	0.00	0.00	0.00	3.62	UNK_AA756546	AA756546
115110_at	0.00	0.00	0.00	0.00	0.00	2.93	UNK_AA250358	AA250358
115114_at	0.00	0.00	0.00	0.00	0.00	3.74	UNK_AW047112	AW047112
115202_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.05***	***UNK_AI851969***	***AI851969***
115398_at	0.00	0.00	0.00	0.00	0.00	2.07	UNK_AA990038	AA990038
115612_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***9.42***	***UNK_AA175284***	***AA175284***
115664_at	0.00	0.00	0.00	0.00	0.00	2.15	UNK_AA222756	AA222756
115679_at	0.00	0.00	0.00	0.00	0.00	2.09	UNK_AA174839	AA174839
115692_r_at	0.00	0.00	0.00	0.00	0.00	2.88	UNK_AA396015	AA396015
115741_at	0.00	0.00	0.00	0.00	0.00	2.52	UNK_AW125843	AW125843
116096_at	0.00	0.00	0.00	0.00	0.00	2.33	UNK_AA718043	AA718043
116113_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.05***	***UNK_AI790538***	***AI790538***
116149_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.15***	***UNK_AI155421***	***AI155421***
116337_at	0.00	0.00	0.00	0.00	0.00	3.22	UNK_AI390374	AI390374
116346_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***6.82***	***UNK_AI843913***	***AI843913***
116380_at	0.00	0.00	0.00	0.00	0.00	2.70	UNK_AI227104	AI227104

116408_at	0.00	0.00	0.00	0.00	0.00	3.16	UNK_AI851073	AI851073
116488_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.95***	***UNK_AA178300***	***AA178300***
116489_r_at	0.00	0.00	0.00	0.00	0.00	2.99	UNK_AA178300	AA178300
116526_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***8.92***	***UNK_AW121457***	***AW121457***
116629_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***6.07***	***UNK_AW215503***	***AW215503***
116642_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.54***	***UNK_AI852563***	***AI852563***
116672_at	0.00	0.00	0.00	0.00	0.00	3.31	UNK_AA611861	AA611861
116755_at	0.00	0.00	0.00	0.00	0.00	2.12	UNK_AI835947	AI835947
116786_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***9.07***	***UNK_AI850351***	***AI850351***
116936_f_at	0.00	0.00	0.00	0.00	0.00	2.55	UNK_AI847709	AI847709
117043_at	0.00	0.00	0.00	0.00	0.00	2.19	UNK_AI851915	AI851915
117056_at	0.00	0.00	0.00	0.00	0.00	2.24	UNK_AI837103	AI837103
117120_at	0.00	0.00	0.00	0.00	0.00	3.42	UNK_AW124145	AW124145
117263_at	0.00	0.00	0.00	0.00	0.00	2.90	UNK_AI850544	AI850544
117297_at	0.00	0.00	0.00	0.00	0.00	2.56	UNK_AI846211	AI846211
117302_at	0.00	0.00	0.00	0.00	0.00	2.95	UNK_AI847477	AI847477
128837_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.79***	***UNK_AA726602***	***AA726602***
129125_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.05***	***UNK_AA475062***	***AA475062***
129284_at	0.00	0.00	0.00	0.00	0.00	3.32	UNK_AA154872	AA154872
129320_at	0.00	0.00	0.00	0.00	0.00	3.25	UNK_AI593773	AI593773
130499_at	0.00	-1.75	0.00	0.00	0.00	2.16	UNK_AW108404	AW108404
132374_at	0.00	0.00	0.00	0.00	0.00	2.21	UNK_AI467276	AI467276
133489_f_at	0.00	0.00	0.00	1.65	0.00	2.50	UNK_AI449387	AI449387
133743_at	0.00	0.00	0.00	0.00	0.00	3.92	UNK_AI467607	AI467607
133851_s_at	0.00	0.00	0.00	1.80	0.00	2.39	UNK_AU019736	AU019736
134141_at	0.00	0.00	0.00	0.00	0.00	3.08	UNK_AA189644	AA189644
135248_at	0.00	0.00	0.00	0.00	0.00	3.48	UNK_AI843905	AI843905
135716_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***37.37***	***UNK_AI836970***	***AI836970***
136580_at	0.00	1.40	0.00	2.03	0.00	1.59	UNK_AI428854	AI428854
136798_at	0.00	0.00	0.00	0.00	0.00	2.31	UNK_AI536255	AI536255
137203_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.09***	***UNK_AI661008***	***AI661008***
137569_at	0.00	0.00	0.00	0.00	0.00	2.28	UNK_AI605650	AI605650
139200_at	0.00	0.00	0.00	0.00	0.00	2.05	UNK_AW045408	AW045408
140629_s_at	0.00	0.00	0.00	1.28	0.00	2.38	UNK_AI506220	AI506220
140759_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.94***	***UNK_AI646554***	***AI646554***
140820_at	0.00	0.00	0.00	0.00	0.00	2.91	UNK_AI662586	AI662586
140840_at	0.00	0.00	0.00	0.00	0.00	2.96	UNK_AI791094	AI791094
94079_at	0.00	0.00	0.00	0.00	0.00	2.57	homolog (Drosophila); Pnutl2	X61452
110428_at	0.00	0.00	0.00	1.81	0.00	2.31	UNK_AA797538	AA797538
112746_at	0.00	0.00	0.00	0.00	0.00	2.54	UNK_AW260381	AW260381
102873_at	0.00	0.00	0.00	1.90	0.00	2.96	TAP2	U60091
98859_at	0.00	0.00	0.00	7.40	5.86	101.96	tartrate resistant; Acp5	M99054
99104_at	0.00	-0.86	0.00	0.00	0.00	2.83	ACRP30	U49915
98589_at	0.00	1.38	0.00	2.93	0.00	2.22	differentiation related protein; Adfp	M93275
99559_at	0.00	0.00	0.00	0.00	0.00	2.62	dehydrogenase family 3, subfamily A2; Aldh3a2	U14390
93354_at	0.00	0.00	0.00	0.00	0.00	3.14	Apoc1	Z22661
104155_f_at	0.00	0.00	0.00	0.00	0.00	2.14	transcription factor 3; Atf3	U19118
95744_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***6.19***	***ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha 70 kDa, isoform 2;***	***U13837***

92597_s_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***7.95***	***ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2;***	***U13838***
92598_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.12***	***ATP6B2***	***AI843029***
94532_at	0.00	0.00	0.00	0.00	0.00	2.12	transporting lysosomal (vacuolar proton pump), 32 kDa; Atp6e	U13841
103205_at	0.00	0.00	0.00	7.48	7.29	36.60	ATP6I	AI286861
130186_f_at	0.00	0.00	0.00	0.00	0.00	2.13	ATP6I	AW211999
96919_at	0.00	0.00	0.00	0.00	0.00	2.22	vacuolar proton channel; Atpl	M64298
94043_at	0.00	0.00	0.00	0.00	0.00	2.47	ATP6S1	AB031290
112716_at	0.00	0.00	0.00	0.00	0.00	2.06	UNK_AW122682	AW122682
94189_at	0.00	0.00	0.00	0.00	0.00	2.17	BAZF	AB011665
100336_s_at	0.00	0.00	0.00	0.00	7.91	53.48	BGLAP1	L24431
93605_r_at	***-1.20***	***0.00***	***0.00***	***0.00***	***0.00***	***4.12***	***BL2***	***AF061260***
92982_at	0.00	0.00	0.00	0.00	0.00	2.65	bone morphogenetic protein 8a; Bmp8a	M97017
96255_at	0.00	0.00	0.00	0.00	0.00	2.02	BNIP3L	AF067395
92668_at	0.00	2.99	1.99	1.78	0.00	3.12	agammaglobulinemia tyrosine kinase; Btk	L10627
106304_at	0.00	0.00	0.00	0.00	0.00	2.83	C1S	AW215831
112110_at	0.00	0.00	0.00	0.00	0.00	2.07	CAMKK	AI843712
92642_at	0.00	0.00	-2.16	0.00	-2.62	5.27	CAR2	M25944
102905_at	0.00	1.80	0.00	2.52	0.00	1.94	CASP11	Y13089
98437_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***7.81***	***CASP3***	***U63720***
98498_at	0.00	0.00	0.00	1.75	0.00	2.28	CASP7	D86353
97832_at	0.00	0.00	0.00	0.00	0.00	2.22	CD97	AA754887
98447_at	0.00	1.36	1.37	1.74	0.00	2.25	binding protein (C/EBP), alpha; Cebpa	M62362
114787_at	0.00	0.00	0.00	0.00	0.00	2.46	UNK_AW107224	AW107224
102027_s_at	0.00	0.00	0.00	0.00	0.00	2.16	CHETK	AA204010
92694_at	2.21	2.77	2.17	0.00	0.00	3.52	Chi3l3	M94584
99070_at	0.00	0.00	1.95	2.74	0.00	2.05	conserved helix-loop-helix ubiquitous kinase; Chuk	U12473
137242_f_at	0.00	0.00	0.00	0.00	0.00	27.84	CKB	AI836689
93595_at	0.00	0.00	0.00	0.00	0.00	2.11	CLN2	AF111172
99413_at	2.76	5.61	2.96	3.04	2.59	16.03	CMKBR1	U29678
134879_at	0.00	0.00	0.00	0.00	0.00	2.62	COL11A2	AI324726
98782_at	0.00	0.00	0.00	0.00	0.00	2.10	complexin 2; Cplx2	D38613
93198_at	0.00	0.00	0.00	0.00	0.00	3.45	colony stimulating factor 3 receptor (granulocyte); Csf3r	M58288
95608_at	0.00	1.92	2.08	3.00	0.00	2.77	CTSB	AI851255
104696_at	0.00	0.00	0.00	0.00	0.00	2.99	CTSE	AJ009840
97336_at	0.00	-2.65	0.00	0.00	0.00	2.12	UNK_AJ131851	AJ131851
100069_at	0.00	0.00	0.00	0.00	0.00	3.27	cytochrome P450, 2f2; Cyp2f2	M77497
97526_at	0.00	0.00	0.00	0.00	0.00	2.67	LOC55946	AW123294
101960_at	0.00	0.00	0.00	2.59	0.00	1.98	D10WSU52E	AI842208
114696_at	0.00	0.00	0.00	0.00	0.00	2.72	UNK_AW046335	AW046335
112306_at	0.00	0.00	0.00	0.00	0.00	2.37	UNK_AW121212	AW121212

92610_at	0.00	0.00	0.00	2.19	0.00	2.64	DNA segment, Chr 17, human D6S45; D17H6S45	M21332
104391_s_at	0.00	0.00	0.00	0.00	0.00	2.95	D17WSU51E	AI850563
115816_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.54***	***UNK_AA869817***	***AA869817***
103877_at	0.00	0.00	0.00	0.00	0.00	2.28	D2WSU58E	AW060485
99143_at	0.00	0.00	0.00	0.00	0.00	2.35	TTGN1	AA614914
113046_at	0.00	0.00	0.00	0.00	0.00	2.45	TTGN1	AI842091
96561_at	0.00	0.00	0.00	0.00	0.00	2.30	UNK_AI157475	AI157475
108293_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.29***	***UNK_AI592230***	***AI592230***
97863_at	0.00	0.00	0.00	0.00	0.00	2.09	UNK_AW125274	AW125274
110406_at	0.00	0.00	0.00	0.00	0.00	2.63	UNK_AA958839	AA958839
99506_at	0.00	0.00	0.00	0.00	0.00	2.25	DAPK2	AB018002
99025_at	0.00	0.00	0.00	0.00	0.00	3.32	Ala-Asp/His) box polypeptide 19; Ddx19	L25125
104371_at	0.00	0.00	0.00	0.00	0.00	2.06	DGAT	AF078752
99881_at	0.00	0.00	0.00	0.00	0.00	3.49	DKK1	AF030433
99328_at	0.00	0.00	0.00	0.00	0.00	3.37	distal-less homeobox 3; Dlx3	U79738
99903_at	0.00	0.00	0.00	0.00	9.98	51.29	DMP1	AJ242625
114809_at	0.00	0.00	0.00	0.00	0.00	3.58	DOKL-PENDING	AW046136
94052_at	0.00	0.00	0.00	0.00	0.00	2.34	DPM2	AB013360
92535_at	0.00	0.00	0.00	0.00	0.00	3.27	Ebf	L12147
104492_at	0.00	0.00	0.00	0.00	0.00	2.18	early B-cell factor 3; Ebf3	U92702
102996_at	0.00	0.00	0.00	0.00	0.00	2.11	lysine-rich leukemia gene; Ell	U80227
92207_at	0.00	0.00	0.00	0.00	0.00	3.03	elastin; Eln	U08210
107900_at	0.00	0.00	0.00	2.56	0.00	2.12	UNK_AW123554	AW123554
102771_at	0.00	0.00	0.00	0.00	0.00	2.62	ESET	AF091628
107996_at	0.00	0.00	0.00	0.00	0.00	2.27	ESTM573010	AW049050
92267_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.46***	***F2R***	***L03529***
94307_at	0.00	0.00	0.00	0.00	0.00	3.38	fibulin 1; Fbln1	X70854
100928_at	-4.16	0.00	0.00	2.21	-0.01	19.58	fibulin 2; Fbln2	X75285
102366_at	0.00	0.00	-5.06	-3.75	0.00	2.31	UNK_AA718169	AA718169
95295_s_at	0.00	0.00	0.00	0.00	0.00	2.74	FMS-like tyrosine kinase 3; Flt3	X59398
101422_at	0.00	0.00	0.00	0.00	0.00	2.07	FNBP4	AW121377
92959_at	0.00	0.00	0.00	0.00	0.00	2.21	B-cell src-homology tyrosine kinase; Frk	Z48757
102016_at	0.00	-1.46	0.00	0.00	0.00	3.68	fat specific gene 27; Fsp27	M61737
94966_at	0.00	1.70	0.00	1.97	0.00	2.99	phosphate dehydrogenase X-linked; G6pdx	Z11911
100407_at	0.00	0.00	0.00	0.00	0.00	2.99	galanin; Gal	L38580
96998_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***7.44***	***UNK_AJ133523***	***AJ133523***
94813_at	0.00	0.00	0.00	0.00	0.00	2.85	growth arrest specific 1; Gas1	X65128
104597_at	0.00	0.00	3.30	2.90	0.00	6.62	GBP2	AJ007970
104134_at	0.00	0.00	0.00	0.00	0.00	2.51	GDAP2	Y17851
92534_at	0.00	0.00	0.00	0.00	0.00	2.86	(gene overexpressed in skeletal muscle);	U10551
102968_at	0.00	0.00	0.00	0.00	0.00	3.69	GGTLA1	AF077765
97384_at	0.00	2.67	3.42	0.00	0.00	2.09	UNK_AA791012	AA791012

100514_at	0.00	0.00	0.00	0.00	0.00	2.43	guanine nucleotide binding protein, alpha 13; Gna13	M63660
93080_at	0.00	0.00	0.00	0.00	0.00	3.13	GNG3LG	AF069954
97385_at	0.00	0.00	0.00	0.00	0.00	2.76	GNK-PENDING	AJ242909
100565_at	0.00	1.93	2.25	2.33	0.00	2.45	GNPI	AW123396
96553_at	0.00	2.13	3.60	0.00	0.00	1.56	G-protein coupled receptor 25; Gpcr25	U39827
100594_at	0.00	0.00	0.00	2.29	0.00	2.00	glycosylphosphatidyl inositol 1 homolog (human); Gpi1h	AB008895
104256_at	1.79	1.75	0.00	0.00	0.00	2.53	UNK_AI120844	AI120844
102995_s_at	0.00	0.00	0.00	0.00	0.00	2.21	GZMA	M13226
93092_at	0.00	1.49	0.00	0.00	0.00	4.62	histocompatibility 2, class II, locus DMa,histocompatibility 2, class II, locus Mb1,histocompatibility 2, class II, locus Mb2,proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2); H2-DMa,H2-DMb1,H2-	U35323
93120_f_at	0.00	0.00	0.00	2.02	0.00	2.69	H2-K	V00746
101876_s_at	0.00	0.00	1.96	2.42	0.00	2.64	UNK_M35247	M35247
98284_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.93***	***H2-T18***	***X03052***
101523_at	0.00	0.00	0.00	2.34	0.00	1.86	H3F3A	AW046194
111423_at	0.00	0.00	0.00	0.00	0.00	3.30	UNK_AI852812	AI852812
100966_at	0.00	0.00	0.00	0.00	0.00	3.32	Hcf2	U07425
104194_at	0.00	0.00	0.00	0.00	0.00	2.51	HEPH	AF082567
104502_f_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.35***	***HES6***	***AI414025***
107620_at	0.00	0.00	0.00	0.00	0.00	2.16	HIPK1	AW125573
98038_at	0.00	0.00	0.00	2.31	0.00	3.06	HMG4	AF022465
93378_at	0.00	0.00	0.00	0.00	0.00	3.93	Hoxc8	X07439
103835_f_at	0.00	0.00	0.00	0.00	0.00	3.00	HPCAL1	AF085192
98962_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.30***	***hepatic lipase; Hpl***	***X58426***
96144_at	0.00	0.00	0.00	0.00	0.00	2.40	IDB4	AJ001972
104500_at	0.00	0.00	0.00	0.00	0.00	2.01	Idua	L34111
92773_at	0.00	0.00	0.00	1.95	0.00	2.30	IER5	AF079528
97409_at	0.00	0.00	2.03	3.55	0.00	2.64	interferon inducible protein 1; Ifi1	U19119
93321_at	0.00	0.00	0.00	2.88	0.00	2.59	interferon activated gene 203; Ifi203	AF022371
103963_f_at	0.00	0.00	6.13	0.00	0.00	12.91	UNK_AA914345	AA914345
137251_f_at	0.00	0.00	0.00	0.00	0.00	3.68	UNK_AI449282	AI449282
94398_s_at	0.00	0.00	0.00	0.00	0.00	2.79	INPP5B	AF040094
99034_at	0.00	0.00	0.00	0.00	0.00	2.23	IRX3	Y15001
98828_at	1.64	3.70	0.00	1.93	0.00	1.84	integrin alpha M (Cd11b); Itgam	X07640
99904_at	0.00	0.00	0.00	0.00	0.00	2.18	ITGB3	AF026509
100906_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.05***	***ITGB7***	***M68903***
99577_at	0.00	0.00	0.00	0.00	0.00	2.21	KITL	M57647
97761_f_at	0.00	0.00	0.00	0.00	0.00	2.29	killer cell lectin-like receptor, subfamily A, member 7; Klra7	U10094
97762_f_at	0.00	0.00	0.00	0.00	0.00	2.56	KLRA7	U12890

99993_at	0.00	0.00	0.00	0.00	0.00	2.25	leucine arylaminopeptidase 1, intestinal; Lap1	U77083
104658_at	0.00	0.00	0.00	0.00	1.22	12.86	LIFR	D17444
96810_at	0.00	0.00	0.00	0.00	0.00	2.15	LMO2	AI154017
97980_at	0.00	0.00	0.00	0.00	0.00	2.54	LTBR	L38423
92401_at	0.00	0.00	0.00	0.00	0.00	2.01	leukotriene C4 synthase; Ltc4s	U27195
96089_at	0.00	0.00	0.00	0.00	0.00	2.20	UNK_AI255972	AI255972
93454_at	0.00	1.58	0.00	2.37	0.00	2.17	LY68	AF081789
92216_at	4.83	3.87	2.49	0.00	0.00	1.72	MADH7	AF015260
103020_s_at	0.00	0.00	0.00	0.00	0.00	2.15	MAP3K1	AI317205
101834_at	0.00	0.00	0.00	2.51	0.00	3.21	protein kinase 3; Mapk3	Z14249
96003_at	0.00	0.00	0.00	0.00	0.00	2.67	MATA1L1	AW048332
96310_at	0.00	0.00	0.00	0.00	0.00	2.98	MBP	L07508
101070_at	0.00	0.00	0.00	0.00	0.00	2.92	MKRN1	AW125438
100484_at	0.00	0.00	0.00	1.38	21.43	135.83	metalloproteinase 13; Mmp13	X66473
100414_s_at	0.00	0.00	-1.84	0.00	0.00	2.69	MPO	X15313
97719_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***9.46***	***RON***	***X74736***
95340_at	0.00	0.00	0.00	0.00	0.00	3.06	Mt3	M93310
102096_f_at	0.00	0.00	-2.42	0.00	0.00	3.13	MUP1	AI255271
101909_f_at	0.00	0.00	-4.14	0.00	0.00	3.70	MUP3	M16357
101910_f_at	0.00	0.00	0.00	0.00	0.00	3.19	major urinary protein 3; Mup3	M16359
101682_f_at	0.00	0.00	0.00	0.00	0.00	3.68	major urinary protein 4; Mup4	M16358
94122_at	7.47	3.44	2.58	0.00	-3.81	-1.94	MYOC	AF041335
103662_at	2.05	2.83	5.66	5.71	0.00	5.18	neutrophil cytosolic factor 4; Ncf4	U59488
97843_at	0.00	0.00	0.00	0.00	0.00	2.39	UNK_AI834866	AI834866
101554_at	0.00	0.00	0.00	9.53	0.00	3.44	NFKBIA	U57524
104149_at	0.00	0.00	0.00	1.87	0.00	2.95	NFKBIA	AI642048
100120_at	0.00	0.00	0.00	0.00	0.00	2.41	NID1	L17324
94982_f_at	0.00	0.00	0.00	0.00	0.00	2.13	UNK_AI852470	AI852470
97497_at	0.00	0.00	0.00	0.00	0.00	3.34	1, (Drosophila); Notch1	Z11886
95016_at	0.00	1.82	1.85	2.13	0.00	2.03	neuropilin; Nrp	D50086
100436_at	0.00	0.00	0.00	0.00	0.00	2.35	Orm1	M27008
103029_at	0.00	0.00	0.00	0.00	0.00	2.74	programmed cell death 4; Pdcd4	D86344
95040_at	0.00	0.00	0.00	0.00	0.00	2.02	UNK_AI840810	AI840810
95079_at	0.00	0.00	0.00	0.00	0.00	3.53	PDGFRA	M57683
93039_at	0.00	0.00	0.00	0.00	0.00	2.50	HLS2	AF009513
96502_at	0.00	0.00	0.00	0.00	0.00	2.85	regulating neutral endopeptidases on the X chromosome; Phex	U75646
130145_i_at	0.00	0.00	0.00	0.00	1.36	25.36	PHEX	AI481510
130146_f_at	0.00	0.00	0.00	0.00	1.68	14.49	PHEX	AI481510
103573_at	0.00	0.00	0.00	0.00	0.00	3.43	4-phosphate 5-kinase, type 1 alpha; Pip5k1a	D86176
101865_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.51***	***PIP5K2A***	***AB009615***
99510_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.15***	***PKCB***	***X59274***
99916_at	0.00	0.00	0.00	0.00	0.00	3.44	protein kinase C, eta; Pkch	D90242
100707_at	0.00	0.00	0.00	0.00	0.00	2.05	UNK_AF030131	AF030131

97926_s_at	0.00	0.00	2.13	0.00	0.00	2.82	PPARG	U10374
113154_at	0.43	0.00	-2.71	-1.11	-2.08	2.44	UNK_AI854500	AI854500
92904_at	0.00	0.00	0.00	0.00	0.00	3.09	containing 1, with ZNF domain; Prdm1	U08185
110362_at	0.00	0.00	0.00	0.00	0.00	2.90	UNK_AW046410	AW046410
94085_at	0.00	0.00	0.00	0.00	0.00	2.37	PRG	M34603
96957_at	0.00	0.00	0.00	0.00	0.00	3.05	PENDING	AB006463
94454_at	0.00	0.00	0.00	2.36	0.00	1.70	PRTB	AF085348
101486_at	0.00	0.00	0.00	0.00	0.00	2.88	PSMB10	Y10875
93085_at	0.00	3.16	6.20	5.37	0.00	6.03	PSMB9	D44456
112345_at	0.00	0.00	0.00	0.00	0.00	2.81	UNK_AI841610	AI841610
92356_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.19***	***phosphatase, non-receptor type 8; Ptpn8***	***M90388***
101932_at	0.00	0.00	0.00	2.02	0.00	3.46	PTPRE	D83484
92309_i_at	0.00	0.00	0.00	0.00	0.00	2.50	phosphatase, receptor-type, M; Ptprm	X58287
92854_at	0.00	1.77	0.00	2.37	0.00	1.82	RAS oncogene family; Rab11a	D50500
100459_at	0.00	0.00	0.00	0.00	0.00	2.57	RAD50 homolog (S. cerevisiae); Rad50	U66887
99032_at	0.00	0.00	0.00	0.00	0.00	2.73	dexamethasone-induced 1; Rasd1	AF009246
104618_at	0.00	0.00	0.00	0.00	0.00	2.22	RBBP9	AI845819
97848_at	0.00	0.00	0.00	0.00	0.00	2.19	RBMX	AJ237846
100530_at	0.00	0.00	0.00	0.00	0.00	2.57	nucleotide dissociation stimulator; Rgds	L07924
97844_at	0.00	0.00	2.15	2.25	0.00	3.16	protein signaling 2; Rgs2	U67187
102762_r_at	0.00	0.00	0.00	0.00	0.00	2.08	RHAG	AF057527
100980_at	0.00	0.00	0.00	0.00	0.00	2.13	Rho-associated coiled-coil forming kinase 1; Rock1	U58512
93839_at	0.00	0.00	0.00	0.00	0.00	2.28	RTN3	AI854888
102336_at	0.00	0.00	0.00	0.00	0.00	2.06	RW1	AF060565
103448_at	0.00	2.51	-4.75	-1.37	-6.47	3.81	binding protein A8 (calgranulin A); S100a8	M83218
103887_at	4.41	0.00	-8.99	-5.52	-6.50	5.43	binding protein A9 (calgranulin B); S100a9	M83219
103715_at	0.00	0.00	0.00	0.00	0.00	3.21	scinderin; Scin	U04354
101436_at	0.00	0.00	3.77	3.82	0.00	6.09	cytokine B subfamily (Cys-X-Cys), member 9; Scyb9	M34815
100112_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***5.61***	***derived factor 1; Sdf1***	***L12030***
103488_at	0.00	1.89	2.03	2.49	0.00	6.53	selectin) ligand; Selpl	X91144
92469_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***6.76***	***SFRP4***	***AF117709***
96126_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.16***	***SGPL1***	***AF036894***
96682_at	0.00	0.00	0.00	0.00	0.00	3.69	SIAT7D	Y15780
102318_at	0.00	0.00	0.00	0.00	0.00	3.68	sialyltransferase 8 (alpha-2, 8-sialytransferase) D; Siat8d	X86000
110381_at	0.00	0.00	0.00	1.54	0.00	2.32	SLAP	AI120030

92582_at	0.00	0.00	0.00	0.00	0.00	2.81	solute carrier family 1, member 7; Slc1a7	L42115
103347_at	0.00	0.00	0.00	0.00	0.00	2.45	UNK_AI852548	AI852548
109069_at	0.00	-2.82	-2.00	0.00	0.00	3.28	SLC39A1	AI255982
98299_s_at	2.97	0.00	0.00	2.13	0.00	1.52	SLFN3	AF099974
115731_at	0.00	0.00	0.00	0.00	0.00	2.37	UNK_AA896535	AA896535
100422_i_at	0.00	0.00	0.00	0.00	0.00	2.96	STAT5A	AJ237939
93680_at	0.00	0.00	0.00	0.00	0.00	2.99	STK10	D89728
100425_at	0.00	1.48	0.00	0.00	0.00	3.69	SYK	U25685
95066_at	0.00	0.00	0.00	0.00	0.00	2.20	Taldo1	U67611
103328_at	0.00	0.00	0.00	2.54	0.00	2.23	TANK	U59864
98087_at	0.00	0.00	0.00	1.88	0.00	2.80	UNK_AW048562	AW048562
92387_at	0.00	0.00	0.00	0.00	0.00	2.03	synthase 1, platelet; Tbxas1	L18868
103539_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***4.07***	***cytoplasmic tyrosine kinase, Dscr28C related (Drosophila); Tec***	***X55663***
92427_at	0.00	0.00	0.00	0.00	0.00	2.71	transforming growth factor, beta receptor I; Tgfbr1	D25540
102637_at	***0.00***	***0.00***	***0.00***	***0.00***	***0.00***	***6.10***	***TGFBR3***	***AF039601***
113920_at	-1.60	0.00	0.00	0.00	0.00	2.12	UNK_AI021069	AI021069
102906_at	0.00	0.00	2.95	3.25	0.00	9.29	T-cell specific GTPase; Tgtp	L38444
99602_at	0.00	1.29	0.00	2.02	0.00	1.67	TIEG	AF064088
101964_at	0.00	0.00	-2.16	0.00	0.00	3.47	transketolase; Tkt	U05809
97893_at	0.00	0.00	0.00	0.00	0.00	2.01	TLP	AB017697
111478_at	0.00	0.00	0.00	1.96	0.00	2.34	UNK_AI047601	AI047601
96700_r_at	0.00	0.00	0.00	0.00	0.00	2.46	UBL1A2-PENDING	AW060594
99580_s_at	0.00	1.50	0.00	1.61	0.00	2.44	UGT1A1	U16818
92760_at	0.00	5.57	3.44	0.00	0.00	4.76	WASP	U42471
94704_at	2.27	0.00	0.00	0.00	0.00	9.98	WISP2	AF100778
97950_at	0.00	0.00	0.00	2.32	0.00	2.77	xanthine dehydrogenase; Xdh	X75129
98053_at	0.00	1.87	0.00	2.77	0.00	2.11	YWHAB	AF058797
97060_at	0.00	0.00	0.00	0.00	0.00	2.95	YWHAQ	AW215489
93013_at	3.57	3.97	3.52	5.65	7.05	6.32	IDB2	AF077861
96331_at	2.04	2.99	2.67	3.12	2.54	2.59	UNK_AI842754	AI842754
99051_at	2.16	3.59	4.32	7.61	3.35	4.76	S100A4	M36579
102104_f_at	2.36	3.77	6.03	8.42	3.97	5.52	UNK_AI504305	AI504305
109403_at	2.15	3.73	5.34	10.02	4.37	19.28	UNK_AW121933	AW121933
114810_at	2.97	9.08	11.55	9.62	8.54	4.12	UNK_AI447446	AI447446
130509_at	2.64	4.77	7.87	6.94	2.24	2.18	UNK_AI851996	AI851996
92810_at	0.00	3.05	4.26	5.46	10.73	9.24	UNK_AI842259	AI842259
92850_at	0.00	2.42	2.43	6.71	9.75	6.66	UNK_AI836446	AI836446
93548_at	0.00	2.61	2.07	3.67	4.32	2.86	UNK_AW122942	AW122942
93829_at	0.00	2.05	3.42	3.58	3.28	5.01	UNK_AW107884	AW107884
93842_at	0.00	2.97	3.69	7.34	12.44	11.01	UNK_AI196645	AI196645
94792_at	3.10	5.07	4.52	4.71	2.76	0.00	UNK_AI447305	AI447305
95102_at	0.00	2.19	2.59	3.61	3.09	3.88	UNK_AW123754	AW123754
95152_g_at	0.00	3.22	2.73	3.00	4.27	4.52	UNK_AW061307	AW061307
95417_at	0.00	2.59	3.27	3.18	3.80	3.54	UNK_AI117848	AI117848
95466_at	0.00	5.84	6.73	4.76	5.82	4.94	UNK_AI837006	AI837006
95542_at	0.00	2.62	2.69	4.54	5.75	4.80	UNK_AI835858	AI835858
95543_at	0.00	3.08	3.87	4.77	4.36	4.23	UNK_AI843046	AI843046
95647_f_at	0.00	2.65	2.69	3.32	3.84	4.28	UNK_AI465845	AI465845
95654_at	0.00	3.23	3.45	5.80	4.72	5.58	UNK_AF109905	AF109905
95673_s_at	0.00	2.31	2.83	5.79	6.60	5.31	UNK_AW124113	AW124113

95749_at	0.00	2.30	2.14	5.13	4.36	3.10	UNK_AW122364	AW122364
95940_f_at	1.92	3.66	5.69	6.58	4.38	7.39	UNK_AW047237	AW047237
96135_at	0.00	2.38	3.85	7.06	6.16	10.09	UNK_AA833425	AA833425
96168_at	0.00	3.47	4.05	3.80	5.45	3.82	UNK_AI591702	AI591702
96319_at	0.00	5.82	5.05	13.49	5.11	6.19	UNK_AW061324	AW061324
96333_g_at	0.00	2.97	2.46	3.17	2.53	2.19	UNK_AW259199	AW259199
96784_at	0.00	4.17	5.63	6.89	5.90	3.14	UNK_AW123269	AW123269
96811_at	1.20	4.20	5.77	6.75	9.85	12.17	UNK_AW049806	AW049806
96834_at	0.00	2.06	2.03	3.08	3.82	4.91	UNK_AI843586	AI843586
96885_at	0.00	5.55	6.66	17.42	21.15	8.95	UNK_AW122271	AW122271
96886_at	0.00	3.53	3.88	3.89	3.05	3.28	UNK_AW060556	AW060556
97444_at	0.00	4.08	4.33	11.02	8.47	20.65	UNK_AI844520	AI844520
97527_at	0.00	4.63	5.52	9.52	8.69	5.59	UNK_AA681998	AA681998
97838_at	0.00	2.19	3.16	3.46	5.45	3.88	UNK_AA684508	AA684508
98076_at	0.00	2.21	3.02	6.55	5.41	5.24	UNK_AI835644	AI835644
98915_at	0.00	5.42	4.17	5.26	4.08	4.94	UNK_AI849082	AI849082
99849_at	0.00	2.58	2.39	3.64	2.12	4.11	UNK_C85523	C85523
100116_at	0.00	3.92	4.43	5.52	8.26	3.36	UNK_AI122538	AI122538
100511_at	0.00	3.60	4.84	3.90	2.10	3.63	UNK_AI154249	AI154249
101061_at	0.00	2.33	2.52	5.11	5.20	4.85	UNK_AI845293	AI845293
101464_at	1.63	7.86	6.79	16.41	14.96	19.13	metalloproteinase; Timp	V00755
101912_at	0.00	4.12	4.68	7.62	13.31	6.66	UNK_AI019679	AI019679
101956_at	0.00	4.37	3.27	7.15	8.46	8.94	UNK_AI834849	AI834849
102056_f_at	0.00	2.01	2.37	3.49	4.61	4.59	UNK_AA839379	AA839379
102108_f_at	0.00	2.23	2.51	3.59	3.19	3.25	UNK_AI505453	AI505453
102907_at	0.00	2.60	6.00	11.32	13.64	4.29	UNK_AW125043	AW125043
103017_at	0.00	2.12	3.20	5.24	4.49	20.95	D13ABB1E	AI060729
103723_at	0.00	2.32	2.67	3.04	3.60	3.21	0	AA608387
104023_at	0.00	2.89	3.42	5.91	4.20	5.95	UNK_AW060457	AW060457
104389_at	0.00	2.65	3.70	4.62	5.54	7.36	UNK_AW049360	AW049360
104464_s_at	0.00	2.24	3.48	10.84	18.75	9.30	UNK_AI642389	AI642389
105606_at	1.75	2.68	2.44	2.77	6.16	5.68	UNK_AW210072	AW210072
105881_at	0.00	2.16	2.37	3.53	5.35	24.32	UNK_AI847606	AI847606
106310_at	0.00	3.45	3.22	2.71	2.82	3.11	UNK_AI843606	AI843606
106619_at	2.41	2.32	0.00	2.78	3.02	3.67	UNK_AW060770	AW060770
107510_at	0.00	8.81	6.27	8.47	8.55	5.39	UNK_AW049506	AW049506
107935_at	0.00	2.29	4.62	10.35	26.40	9.69	UNK_AI450518	AI450518
108018_at	0.00	2.98	3.50	5.18	16.34	11.82	UNK_AA959436	AA959436
108477_at	0.00	3.49	3.67	6.12	15.44	10.74	UNK_AA692253	AA692253
109103_f_at	0.00	2.58	3.05	3.95	4.48	3.00	UNK_AI841088	AI841088
109669_at	0.00	2.64	3.10	5.19	15.50	11.17	UNK_AA796759	AA796759
109737_at	0.00	3.30	3.69	7.52	10.54	18.42	UNK_AI836805	AI836805
109982_at	0.00	3.10	2.97	3.92	5.94	12.35	UNK_AI851247	AI851247
110160_at	0.00	3.54	6.56	5.47	2.73	3.51	UNK_AI510217	AI510217
110187_at	0.00	2.20	2.36	2.56	2.44	3.74	UNK_AA624041	AA624041
110334_at	0.00	2.05	2.27	6.10	4.52	6.30	UNK_AI852289	AI852289
110848_at	0.00	3.74	4.17	8.73	18.05	9.18	UNK_AI851487	AI851487
111125_at	0.00	2.32	2.83	2.54	3.64	7.94	UNK_AI391368	AI391368
111225_at	0.00	2.83	2.56	3.59	6.73	3.30	UNK_AW121825	AW121825
111350_at	0.00	2.33	3.71	2.48	5.40	4.17	UNK_AI462022	AI462022
111841_at	0.00	3.34	4.66	5.84	4.01	7.21	UNK_AI527656	AI527656
112039_at	0.00	2.69	2.34	2.25	2.25	3.88	UNK_AA178128	AA178128
112322_at	0.00	3.84	2.74	2.31	2.17	3.75	UNK_AA931004	AA931004
112383_at	0.00	2.92	5.72	9.18	4.14	6.63	UNK_AI155444	AI155444
112687_at	0.00	2.10	2.91	2.49	3.33	3.44	UNK_AA683840	AA683840
112763_at	0.00	3.08	2.52	3.95	5.44	2.31	UNK_AI788757	AI788757
112807_at	0.00	2.55	3.32	3.33	5.30	3.44	UNK_AI891565	AI891565
113750_at	1.90	3.09	3.33	3.67	2.95	4.78	UNK_AA881110	AA881110

113932_g_at	0.00	3.21	3.06	5.89	6.81	3.86	UNK_AW230677	AW230677
114025_at	1.61	6.05	10.16	14.50	25.81	11.77	UNK_AI643935	AI643935
114303_at	1.50	8.14	14.58	11.85	13.19	2.02	UNK_AW107218	AW107218
114498_at	0.00	3.36	3.84	3.78	4.04	3.68	UNK_AW215808	AW215808
114701_at	1.81	2.80	2.37	5.00	12.96	7.64	UNK_AI425702	AI425702
116159_at	0.00	3.76	4.87	3.67	2.28	3.06	UNK_AA823048	AA823048
116414_at	0.00	3.28	3.48	5.32	3.90	7.35	UNK_AI180528	AI180528
116943_at	0.00	2.38	2.30	4.09	3.55	4.14	UNK_AI852450	AI852450
116969_at	0.00	2.04	2.14	2.52	2.63	3.29	UNK_AI843050	AI843050
117049_at	0.00	2.11	2.62	2.33	2.62	3.41	UNK_AI848494	AI848494
135169_at	0.00	2.79	3.47	3.44	2.37	2.14	UNK_AA509929	AA509929
137100_at	2.43	4.34	4.00	4.39	1.80	3.84	UNK_AW214591	AW214591
139422_at	0.00	2.58	3.05	5.10	2.06	3.16	UNK_AW212694	AW212694
92185_at	0.00	0.00	2.80	3.37	5.13	2.63	UNK_AI846023	AI846023
92787_at	0.00	2.76	0.00	2.66	3.64	2.18	UNK_AI845902	AI845902
92800_i_at	0.00	1.89	2.06	3.12	3.93	5.57	UNK_AI836694	AI836694
93037_i_at	0.00	2.22	0.00	3.35	2.89	4.40	LPC1	M69260
93327_at	0.00	0.00	4.87	5.05	4.80	4.81	UNK_AI842665	AI842665
94273_at	0.00	1.93	2.18	4.60	6.39	4.24	UNK_AI849067	AI849067
94330_at	0.00	5.76	2.95	4.18	2.28	0.00	UNK_AA710564	AA710564
94486_at	0.00	1.87	2.21	3.22	3.76	2.56	UNK_AW125178	AW125178
94549_at	0.00	2.24	0.00	2.48	2.75	2.12	UNK_AI315650	AI315650
94830_at	0.00	2.01	0.00	2.55	2.23	2.09	UNK_AI854300	AI854300
94992_at	0.00	1.93	2.08	3.30	5.15	4.11	UNK_AI840667	AI840667
95590_at	0.00	0.00	2.08	3.19	3.55	4.06	UNK_AA615951	AA615951
95648_at	0.00	1.92	2.17	2.65	2.60	3.36	UNK_AA655507	AA655507
95885_at	0.00	1.53	2.21	3.06	3.95	2.16	UNK_AA177621	AA177621
96004_at	0.00	6.08	0.00	5.08	7.87	7.33	UNK_AI851641	AI851641
96262_at	0.00	4.44	3.02	1.84	2.66	3.32	UNK_AI836812	AI836812
96605_at	0.00	1.99	8.89	9.27	26.99	8.68	UNK_AI787183	AI787183
96708_at	0.00	1.59	2.40	3.97	4.47	4.62	UNK_AW120643	AW120643
97211_at	0.00	0.00	2.92	5.48	8.89	5.70	UNK_AI747444	AI747444
97425_at	0.00	3.99	4.68	0.00	15.01	10.66	UNK_AI840191	AI840191
97456_at	0.00	3.00	1.91	3.34	2.85	4.04	UNK_AI838021	AI838021
97811_at	0.00	2.45	0.00	6.99	21.66	12.97	UNK_AI844507	AI844507
97947_at	0.00	1.70	2.19	2.39	2.35	3.32	UNK_AI836959	AI836959
97964_at	0.00	0.00	4.12	10.11	19.39	10.90	UNK_AW122851	AW122851
98107_at	0.00	1.89	2.26	4.29	5.16	5.87	UNK_AW123801	AW123801
98346_at	0.00	0.00	2.40	3.53	8.88	9.07	UNK_AI593759	AI593759
98440_at	0.00	0.00	3.53	3.85	3.62	3.27	UNK_AA596710	AA596710
99149_at	0.00	1.63	2.59	2.83	3.43	2.04	UNK_AI851230	AI851230
99191_at	0.00	1.66	2.04	2.42	2.86	2.36	UNK_AI844939	AI844939
99366_at	0.00	1.74	2.18	2.99	3.04	7.11	UNK_AI553536	AI553536
99505_at	0.00	2.50	0.00	4.22	2.83	2.64	UNK_AI844664	AI844664
100611_at	0.00	1.75	2.16	2.76	2.14	3.06	lysozyme; Lyzs	M21050
102936_at	0.00	2.24	2.95	2.51	2.80	0.00	UNK_AW125314	AW125314
103435_at	0.00	2.05	0.00	4.32	4.31	6.16	UNK_AW045910	AW045910
103525_at	0.00	0.00	2.54	2.48	2.46	2.26	UNK_AA981725	AA981725
103570_at	1.36	0.00	3.57	8.33	32.50	24.51	UNK_AI315647	AI315647
103605_g_at	0.00	2.34	0.00	2.72	3.09	3.43	UNK_AW231026	AW231026
103606_r_at	0.00	0.00	3.31	5.63	5.50	5.04	UNK_AW121438	AW121438
103607_at	0.00	1.91	2.63	4.83	7.58	4.57	UNK_AI882309	AI882309
103905_at	0.00	1.30	2.12	4.42	2.69	2.19	UNK_AI314958	AI314958
104315_at	0.00	0.00	2.66	3.65	5.15	4.85	UNK_AI846773	AI846773
104322_at	0.00	2.76	-0.53	8.24	10.40	4.90	UNK_AI121796	AI121796
104578_f_at	0.00	1.68	2.43	4.41	6.50	5.77	UNK_AI195392	AI195392
104735_at	0.00	1.83	3.51	4.53	7.04	7.68	UNK_AI842065	AI842065
104792_at	0.00	0.00	3.24	2.74	2.85	2.31	UNK_AI504064	AI504064
106007_at	0.00	0.00	2.18	2.81	4.75	4.24	UNK_AA798398	AA798398

106215_at	0.00	2.75	3.03	0.00	3.77	4.25	UNK_AI839767	AI839767
106281_f_at	0.00	0.00	2.58	4.87	12.31	6.40	UNK_AI851600	AI851600
106287_at	0.00	0.00	3.09	3.01	2.93	4.46	UNK_AW124686	AW124686
106984_at	0.00	0.00	4.71	3.16	2.02	3.27	UNK_AA655780	AA655780
107043_at	0.00	2.49	0.00	2.68	4.39	10.55	UNK_AA770975	AA770975
107063_at	0.00	0.00	2.56	4.20	9.80	9.48	UNK_AI852358	AI852358
107406_at	0.00	0.00	2.34	2.06	5.20	3.73	UNK_AW048981	AW048981
107408_at	1.42	2.22	0.00	3.13	4.06	3.64	UNK_AW049048	AW049048
107520_at	0.00	0.00	2.20	2.65	2.60	7.04	UNK_AI846038	AI846038
107917_at	0.00	2.57	0.00	3.20	7.84	6.47	UNK_AA796707	AA796707
108048_at	0.00	0.00	2.60	2.63	5.24	2.87	UNK_AI836268	AI836268
108889_at	0.00	2.27	0.00	2.74	7.67	8.01	UNK_AA870215	AA870215
109021_at	0.00	0.00	4.01	3.06	2.13	3.35	UNK_AW214142	AW214142
109033_at	0.00	2.56	0.00	3.78	6.98	5.70	UNK_AW122053	AW122053
109169_at	0.00	0.00	2.18	2.74	2.66	2.83	UNK_AI841448	AI841448
109330_at	0.00	1.86	2.26	3.04	8.08	4.45	UNK_AI195395	AI195395
109554_at	0.00	3.33	3.40	2.32	1.66	2.64	UNK_AA611111	AA611111
109709_at	0.00	0.00	4.62	6.04	6.21	5.36	UNK_AW124034	AW124034
109989_at	0.00	2.30	0.00	2.23	3.21	2.82	UNK_AW124029	AW124029
110124_at	0.00	1.81	2.27	2.56	2.86	2.77	UNK_AI647471	AI647471
110319_at	0.00	0.00	2.77	3.82	6.37	7.50	UNK_AW215732	AW215732
110351_at	0.00	0.00	2.46	2.37	2.59	3.02	UNK_AI842140	AI842140
110429_at	0.00	0.00	2.59	4.62	5.25	11.50	UNK_AW060321	AW060321
110853_at	0.00	1.86	3.15	3.52	4.37	5.49	UNK_AW124968	AW124968
111044_f_at	0.00	1.72	3.54	3.57	2.88	4.78	UNK_AA175250	AA175250
111229_at	0.00	2.14	0.00	2.59	3.44	3.06	UNK_AW123416	AW123416
111624_at	0.00	0.00	2.65	4.22	4.19	4.97	UNK_AI843542	AI843542
111628_at	0.00	1.82	2.88	2.96	3.56	3.44	UNK_AA415523	AA415523
111680_at	0.00	0.00	3.55	2.66	3.45	4.18	UNK_AA681812	AA681812
111965_at	0.00	1.88	5.19	12.18	16.02	7.92	UNK_AA869027	AA869027
112062_at	0.00	0.00	2.60	4.10	8.79	9.97	UNK_AA989939	AA989939
112349_at	0.00	3.23	0.00	4.74	4.11	7.10	UNK_AW048860	AW048860
112373_at	0.00	3.42	0.00	3.33	3.07	9.92	UNK_AI840826	AI840826
112386_at	0.00	0.00	2.10	6.36	5.47	5.04	UNK_AI838633	AI838633
112411_at	0.00	3.41	0.00	3.71	5.34	5.90	UNK_AW229681	AW229681
112445_at	0.00	4.88	0.00	4.11	5.78	7.36	UNK_AI156718	AI156718
112464_at	0.00	0.00	2.20	2.19	5.18	3.92	UNK_AI194396	AI194396
112465_at	0.00	0.00	3.34	2.83	3.08	4.56	UNK_AI226955	AI226955
112766_at	0.00	0.00	2.32	2.86	4.43	2.35	UNK_AI788798	AI788798
112996_at	0.00	1.91	3.42	3.15	2.25	3.79	UNK_AA170203	AA170203
113036_at	0.00	0.00	9.63	27.96	22.87	15.50	UNK_AW120709	AW120709
113196_at	0.00	0.00	2.73	5.42	19.47	19.66	UNK_AW124306	AW124306
113268_s_at	0.00	0.00	2.94	4.41	4.90	6.78	UNK_AI835128	AI835128
113302_at	0.00	0.00	3.92	4.35	2.37	2.39	UNK_AA967902	AA967902
113322_at	0.00	4.17	3.83	2.29	1.80	3.97	UNK_AI116109	AI116109
113989_at	0.00	1.53	2.26	3.83	2.32	2.71	UNK_AW209554	AW209554
113995_at	0.00	0.00	2.09	3.10	7.68	8.85	UNK_AW061313	AW061313
114602_at	0.00	0.00	2.53	4.43	5.72	4.29	UNK_AW228836	AW228836
114633_at	0.00	1.95	2.18	2.85	2.34	2.13	UNK_AA895405	AA895405
114635_at	0.00	0.00	3.64	5.07	2.28	3.67	UNK_AA960121	AA960121
114849_at	0.00	0.00	2.04	2.51	2.21	2.98	UNK_AI462265	AI462265
115057_at	0.00	3.81	0.00	4.34	6.22	9.28	UNK_AI591439	AI591439
115463_at	0.00	1.89	2.87	3.42	3.47	3.30	UNK_AI118729	AI118729
115786_at	0.00	2.74	4.53	4.67	5.11	0.00	UNK_AI563688	AI563688
115795_at	0.00	1.66	2.14	2.42	2.02	2.38	UNK_AI851830	AI851830
115800_at	0.00	0.00	2.19	2.85	3.72	4.95	UNK_AW125385	AW125385
115840_at	0.00	3.42	0.00	4.03	7.10	8.17	UNK_AA756752	AA756752
116382_at	0.00	2.11	0.00	3.91	8.77	15.59	UNK_AW046112	AW046112
117179_at	0.00	1.97	8.96	15.72	41.33	9.71	UNK_AI852894	AI852894

130969_at	0.00	0.00	2.19	2.47	2.21	3.14	UNK_AI844373	AI844373
135177_at	0.00	3.65	0.00	5.69	3.01	3.18	UNK_AI882074	AI882074
135189_f_at	0.00	0.00	2.54	5.92	8.57	7.44	UNK_AI481498	AI481498
135257_at	0.00	1.76	2.12	3.83	3.13	5.08	UNK_AI848406	AI848406
137034_f_at	0.00	2.01	0.00	3.48	3.35	3.21	UNK_AI480781	AI480781
137656_s_at	2.10	4.17	0.00	3.83	1.46	2.66	UNK_AI195998	AI195998
92268_at	0.00	0.00	0.00	2.96	2.58	2.60	UNK_AI854851	AI854851
92279_at	0.00	0.00	0.00	3.35	3.86	2.45	UNK_AW121320	AW121320
92831_at	0.00	1.64	0.00	2.11	2.74	4.13	UNK_AI846308	AI846308
93174_at	0.00	0.00	0.00	3.77	9.21	14.95	UNK_AI593640	AI593640
93236_s_at	0.00	1.84	2.29	2.54	3.78	1.95	thymidylate synthase; Tyms	M13352
93443_at	0.00	-1.73	0.00	2.28	4.61	2.81	UNK_AW212271	AW212271
93472_at	0.00	0.00	0.00	5.12	7.16	5.99	UNK_AA796989	AA796989
93714_f_at	0.00	0.00	0.00	2.75	2.14	2.74	UNK_AI117211	AI117211
93747_at	0.00	0.00	0.00	2.11	2.53	2.90	UNK_AW122599	AW122599
93830_at	0.00	0.00	0.00	2.26	2.94	2.21	UNK_AI851199	AI851199
93831_at	0.00	0.00	0.00	2.37	3.09	2.39	UNK_AI316087	AI316087
93974_at	0.00	0.00	1.65	4.60	2.63	5.21	33 POLYPEPTIDE [R.NORVEGICUS]	AW212475
93999_at	0.00	1.56	1.86	2.43	2.61	2.30	CD8B	AW060597
94041_at	0.00	0.00	1.71	2.39	2.63	2.32	UNK_AI840643	AI840643
94060_at	0.00	0.00	0.00	2.72	3.43	2.97	UNK_AI852623	AI852623
94289_r_at	0.00	0.00	0.00	5.89	6.92	5.31	UNK_AI851574	AI851574
94415_at	0.00	1.93	0.00	3.04	2.62	2.30	0	AA710439
94445_at	0.00	0.00	0.00	2.05	3.55	3.58	UNK_AW125273	AW125273
94470_i_at	0.00	0.00	0.00	2.09	3.10	3.00	UNK_AW045974	AW045974
94473_at	0.00	0.00	0.00	2.23	2.77	3.60	UNK_AW047951	AW047951
94503_at	0.00	0.00	0.00	5.46	4.11	4.57	UNK_AI842492	AI842492
94511_at	0.00	0.00	1.98	3.57	4.92	3.27	UNK_AI850546	AI850546
94784_at	0.00	0.00	2.33	2.63	2.69	0.00	UNK_AI593484	AI593484
94931_at	0.00	0.00	1.55	2.64	4.46	2.36	UNK_AI851104	AI851104
95020_at	0.00	1.59	0.00	2.17	2.56	3.30	UNK_AI848868	AI848868
95042_at	0.00	0.00	0.00	2.81	3.92	3.09	UNK_AI839770	AI839770
95091_at	0.00	0.00	0.00	2.19	3.07	2.05	UNK_AI839895	AI839895
95151_at	0.00	0.00	1.55	2.53	10.58	4.87	UNK_AW061307	AW061307
95400_i_at	0.00	0.00	0.00	2.02	2.63	3.14	UNK_AI447783	AI447783
95404_at	0.00	0.00	0.00	2.20	2.89	2.95	UNK_AW123453	AW123453
95405_at	0.00	0.00	0.00	2.32	2.36	2.24	UNK_AW045534	AW045534
95609_at	0.00	0.00	1.63	2.66	2.03	2.61	UNK_AA869927	AA869927
95637_at	0.00	0.00	0.00	5.65	6.59	4.70	UNK_AI838592	AI838592
96117_r_at	0.00	1.70	1.72	4.04	6.17	3.16	UNK_AI843732	AI843732
96207_at	0.00	1.93	0.00	2.38	2.45	2.47	UNK_AW046449	AW046449
96249_at	0.00	0.00	0.00	2.41	2.55	2.39	UNK_AW122105	AW122105
96271_at	0.00	0.00	0.00	2.11	2.16	2.61	UNK_AA914105	AA914105
96288_at	0.00	0.00	0.00	2.42	2.50	2.26	UNK_AI648831	AI648831
96524_at	0.00	0.00	0.00	7.01	7.10	6.99	UNK_AI157060	AI157060
96526_at	0.00	0.00	1.78	2.38	4.26	4.98	UNK_AW228840	AW228840
96603_at	0.00	0.00	1.45	3.17	7.47	6.26	UNK_AW123556	AW123556
96610_at	0.00	1.73	0.00	2.37	2.33	3.57	UNK_AW046442	AW046442
96831_at	0.00	0.00	0.00	4.14	9.52	4.49	UNK_AA755004	AA755004
96855_at	0.00	0.00	0.00	4.41	2.28	3.04	UNK_AI839946	AI839946
97322_at	1.42	2.58	4.12	2.93	1.61	1.47	UNK_AI835093	AI835093
97360_at	0.00	0.00	0.00	4.98	8.63	6.80	UNK_AI841689	AI841689
97374_at	0.00	0.00	0.00	4.28	5.95	5.36	UNK_AI840458	AI840458
97387_at	0.00	0.00	0.00	3.29	6.53	6.82	UNK_AI847879	AI847879
97420_at	0.00	1.86	2.49	3.68	2.46	0.00	UNK_AW230891	AW230891
97492_at	0.00	0.00	0.00	2.77	2.23	2.14	UNK_AW121746	AW121746
97496_f_at	0.00	1.85	1.97	3.37	3.29	3.18	UNK_AW048944	AW048944

97711_at	4.97	7.08	9.21	0.00	0.00	-1.58	UNK_AI606967	AI606967
97770_s_at	0.00	0.00	0.00	2.02	2.40	2.53	UNK_AA733372	AA733372
97818_at	0.00	0.00	0.00	2.30	2.75	2.58	UNK_AI838691	AI838691
97885_at	0.00	0.00	0.00	2.89	3.28	3.88	UNK_AB031386	AB031386
97918_at	0.00	0.00	0.00	2.13	2.36	2.81	UNK_AA623587	AA623587
98042_at	0.00	0.00	0.00	4.50	7.72	7.38	UNK_AW049787	AW049787
98083_at	0.00	0.00	0.00	2.45	2.40	2.85	UNK_AW049031	AW049031
98594_at	0.00	0.00	0.00	2.89	4.90	5.86	UNK_AW125453	AW125453
98615_at	0.00	0.00	1.63	2.53	2.51	2.12	UNK_AW049570	AW049570
98917_at	0.00	0.00	0.00	2.09	2.77	3.39	UNK_AA823202	AA823202
98931_at	0.00	0.00	0.00	2.18	2.06	4.22	UNK_AW123589	AW123589
98956_at	0.00	1.91	0.00	4.40	4.62	4.19	UNK_AI844979	AI844979
98975_at	0.00	0.00	0.00	2.13	2.85	3.32	UNK_AI019999	AI019999
99378_f_at	0.00	0.00	0.00	3.06	2.42	4.09	UNK_M18837	M18837
100074_at	0.00	0.00	0.00	4.44	3.57	2.83	UNK_AW046723	AW046723
100100_at	0.00	6.72	5.24	5.35	0.00	0.00	UNK_AA762212	AA762212
100471_at	0.00	0.00	1.84	5.94	20.39	6.44	UNK_AW048916	AW048916
100915_at	0.00	1.46	1.50	3.52	2.39	3.61	UNK_AW125698	AW125698
100974_at	0.00	0.00	2.13	1.44	2.13	3.27	UNK_AI844250	AI844250
101001_at	0.00	0.00	0.00	2.97	4.32	3.67	UNK_AI647612	AI647612
101084_f_at	0.00	0.00	0.00	4.39	4.47	3.59	UNK_AI527477	AI527477
101441_i_at	0.00	0.00	0.00	3.13	2.07	2.48	ITPR5	AF031127
101856_at	0.00	0.00	0.00	2.71	2.82	2.13	UNK_AI836771	AI836771
102279_at	0.00	0.00	1.71	4.39	5.91	9.29	UNK_AW046479	AW046479
102354_at	0.00	1.81	2.65	0.00	3.39	2.56	UNK_AI049398	AI049398
102812_i_at	0.00	0.00	0.00	2.63	2.76	2.35	UNK_AW210346	AW210346
102813_f_at	0.00	0.00	0.00	3.19	3.50	3.42	UNK_AW210346	AW210346
103056_at	0.00	0.00	0.00	2.34	2.20	2.30	UNK_AI849721	AI849721
103071_at	0.00	0.00	2.37	2.05	2.42	0.00	UNK_AI843655	AI843655
103345_at	0.00	0.00	0.00	2.50	5.36	3.40	UNK_AW046708	AW046708
103381_at	0.00	0.00	0.00	3.22	3.91	3.29	UNK_AI838735	AI838735
103491_at	0.00	0.00	0.00	2.34	2.48	3.21	UNK_AA968123	AA968123
103556_at	0.00	0.00	1.92	4.21	4.47	2.64	ARP2-PENDING	AI840158
103708_at	0.00	1.72	2.04	3.24	3.11	0.00	UNK_AI132207	AI132207
103709_at	0.00	0.00	0.00	3.82	2.14	2.74	UNK_AA763466	AA763466
103726_at	0.00	1.67	0.00	3.54	3.48	2.76	UNK_AI842264	AI842264
103748_at	0.00	0.00	3.05	0.00	6.47	4.96	UNK_AW125627	AW125627
103863_at	0.00	1.56	0.00	2.29	2.39	2.32	UNK_AW049769	AW049769
104188_at	0.00	1.72	0.00	3.24	4.10	4.01	UNK_AI853703	AI853703
104250_at	0.00	0.00	0.00	2.04	3.44	3.33	UNK_AW121353	AW121353
104386_f_at	0.00	0.00	0.00	2.79	2.29	4.39	UNK_AI843901	AI843901
104399_at	0.00	1.79	0.00	2.21	2.47	2.45	UNK_AI850965	AI850965
104427_at	0.00	1.64	0.00	2.13	2.42	2.92	UNK_AA930526	AA930526
104435_at	0.00	0.00	0.00	2.52	4.50	4.08	UNK_AI644072	AI644072
104544_at	0.00	1.92	2.25	2.22	2.98	0.00	UNK_AA675604	AA675604
104579_r_at	0.00	1.68	0.00	4.11	3.04	4.02	UNK_AI195392	AI195392
104677_at	0.00	0.00	0.00	2.37	3.06	2.31	UNK_AI852008	AI852008
104766_at	0.00	2.25	0.00	3.53	3.02	1.54	UNK_AI851198	AI851198
105411_at	0.00	1.86	0.00	2.61	4.05	4.05	UNK_AI842846	AI842846
105451_at	0.00	0.00	0.00	3.53	9.33	5.81	UNK_AI153747	AI153747
105585_at	0.00	0.00	0.00	2.17	2.27	2.37	UNK_AI466953	AI466953
106051_at	0.00	0.00	0.00	3.22	11.40	8.03	UNK_AI838192	AI838192
106198_at	0.00	0.00	0.00	2.10	3.50	2.96	UNK_AI847104	AI847104
106222_at	0.00	0.00	0.00	3.02	10.05	8.98	UNK_AW050335	AW050335
106260_at	0.00	0.00	0.00	3.66	5.37	3.81	UNK_AW123372	AW123372
106294_at	0.00	0.00	0.00	2.34	2.47	2.79	UNK_AI834916	AI834916
106469_at	0.00	3.06	2.69	5.69	0.00	0.00	UNK_AI835918	AI835918
106554_at	0.00	0.00	0.00	2.16	2.03	2.55	UNK_AI854833	AI854833
106569_at	0.00	0.00	0.00	2.30	2.04	2.34	UNK_AA611588	AA611588

106581_at	0.00	0.00	0.00	2.22	2.23	2.53	UNK_AW049498	AW049498
106596_at	0.00	0.00	0.00	2.79	2.50	5.15	UNK_AW046788	AW046788
106623_at	0.00	0.00	0.00	3.01	5.89	20.01	UNK_AI180489	AI180489
106638_at	0.00	0.00	0.00	2.26	2.86	5.68	UNK_AA762192	AA762192
107099_at	0.00	0.00	-2.37	3.85	3.65	3.57	UNK_AA792731	AA792731
107124_at	0.00	0.00	2.17	0.00	2.98	2.82	UNK_AI848296	AI848296
107515_at	0.00	0.00	0.00	2.35	5.98	4.81	UNK_AI152665	AI152665
107519_at	0.00	1.66	0.00	2.83	3.62	7.65	UNK_AW122581	AW122581
107521_at	0.00	0.00	0.00	2.38	3.00	3.81	UNK_AI853924	AI853924
107553_at	0.00	0.00	1.28	2.76	3.62	3.25	UNK_AW047590	AW047590
107575_at	0.00	0.00	0.00	3.06	4.02	3.94	UNK_AA980835	AA980835
107587_at	0.00	0.45	0.00	2.13	4.88	3.39	UNK_AI035938	AI035938
107599_at	0.00	0.00	0.00	2.18	2.13	2.08	UNK_AI121363	AI121363
107959_at	0.00	0.00	0.00	2.33	4.89	5.30	UNK_AA980253	AA980253
108008_at	0.00	0.00	2.96	0.00	4.43	7.06	UNK_AI551848	AI551848
108049_at	0.00	0.00	0.00	7.17	8.21	5.99	UNK_AW121296	AW121296
108105_at	0.00	0.00	5.44	4.71	1.58	5.04	UNK_AA839380	AA839380
108382_at	0.00	0.00	0.00	5.21	5.76	6.53	UNK_AW259632	AW259632
108383_at	0.00	0.00	0.00	3.99	5.62	7.43	UNK_AA066623	AA066623
108384_g_at	0.00	0.00	0.00	4.00	6.89	6.79	UNK_AA066623	AA066623
108466_at	0.00	0.00	3.44	0.00	3.36	5.90	UNK_AI596076	AI596076
108532_at	0.00	0.00	0.00	2.66	4.30	3.67	UNK_AW122038	AW122038
108541_at	0.00	0.00	0.00	2.03	2.62	2.82	UNK_AW048008	AW048008
108568_at	0.00	0.00	0.00	2.42	2.63	2.64	UNK_AI155631	AI155631
108820_at	0.00	0.00	0.00	3.58	4.40	3.77	UNK_AW049198	AW049198
109051_at	0.00	0.00	0.00	2.66	4.11	4.07	UNK_AI157102	AI157102
109059_at	0.00	0.00	0.00	2.98	6.09	4.59	UNK_AI594658	AI594658
109090_at	0.00	0.00	2.21	0.00	2.45	2.26	UNK_AA032312	AA032312
109120_at	0.00	0.00	0.00	2.42	5.70	4.73	UNK_AI157108	AI157108
109178_g_at	0.00	0.00	0.00	3.12	3.11	4.12	UNK_AW122327	AW122327
109352_s_at	0.00	0.00	0.00	2.01	2.51	3.11	UNK_AI840133	AI840133
109368_at	0.00	0.00	0.00	2.40	8.63	10.05	UNK_AI840476	AI840476
109387_f_at	0.00	0.00	0.00	2.55	3.54	4.69	UNK_AA960590	AA960590
109553_at	0.00	0.00	0.00	3.76	4.23	5.14	UNK_AI645484	AI645484
109652_at	0.00	0.00	0.00	4.42	10.57	4.83	UNK_AI596121	AI596121
109682_at	0.00	1.47	0.00	2.80	3.58	3.26	UNK_AW046087	AW046087
109722_at	0.00	0.00	0.00	3.76	3.11	5.30	UNK_AI843690	AI843690
109728_at	0.00	0.00	0.00	2.72	3.41	4.91	UNK_AI848741	AI848741
109733_at	0.00	0.00	0.00	2.11	3.48	4.36	UNK_AW121434	AW121434
109757_at	0.00	0.00	0.00	2.45	2.41	5.31	UNK_AW122156	AW122156
110225_at	0.00	0.00	0.00	2.35	3.42	3.96	UNK_AI646302	AI646302
110228_at	0.00	0.00	0.00	3.63	17.05	10.06	UNK_AI197339	AI197339
110318_at	0.00	0.00	0.00	2.36	3.20	7.36	UNK_AA866881	AA866881
110382_at	0.00	0.00	0.00	2.35	2.14	3.23	UNK_AW215580	AW215580
110713_at	0.00	0.00	0.00	2.31	4.34	3.18	UNK_AW124288	AW124288
110728_at	0.00	2.05	2.30	1.91	1.98	2.38	UNK_AA959412	AA959412
110835_at	0.00	0.00	0.00	2.96	3.58	3.92	UNK_AW122399	AW122399
111029_at	0.00	0.00	2.83	2.65	5.89	1.80	UNK_AW060610	AW060610
111272_at	0.00	1.98	0.00	2.45	3.49	3.79	UNK_AI006978	AI006978
111552_at	0.00	5.28	0.00	9.85	3.20	0.00	UNK_AA645952	AA645952
111684_at	0.00	0.00	0.00	4.50	7.26	4.83	UNK_AA856145	AA856145
111816_at	0.00	0.00	0.00	2.08	2.78	3.47	UNK_AI853182	AI853182
111831_at	0.00	0.00	2.34	1.99	2.46	3.35	UNK_AA759455	AA759455
111909_f_at	0.00	0.00	0.00	5.45	5.79	4.68	UNK_AW047813	AW047813
112321_at	0.00	0.00	0.00	2.25	2.63	3.38	UNK_AA198542	AA198542
112350_at	0.00	0.00	0.00	2.05	3.09	3.70	UNK_AA739089	AA739089
112375_at	0.00	0.00	0.00	2.44	3.43	3.62	UNK_AI850477	AI850477
112379_at	0.00	0.00	2.65	0.00	4.96	3.46	UNK_AI851953	AI851953
112394_at	0.00	1.50	1.92	2.81	3.97	5.52	UNK_AI790592	AI790592

112453_at	0.00	0.00	0.00	3.38	3.38	5.27	UNK_AW048464	AW048464
112509_at	0.00	0.00	0.00	2.47	9.02	2.08	UNK_AW125633	AW125633
112661_at	0.00	0.00	0.00	3.24	3.61	3.86	UNK_AI877116	AI877116
112679_at	0.00	0.00	6.56	5.10	4.31	0.00	UNK_AA867783	AA867783
112684_at	0.00	0.00	0.00	2.54	2.50	2.46	UNK_AI853966	AI853966
112831_at	0.00	0.00	0.00	6.83	5.69	5.51	UNK_AI845409	AI845409
112910_f_at	0.00	0.00	0.00	2.28	10.24	2.63	UNK_AW229261	AW229261
112922_i_at	0.00	0.00	0.00	5.39	12.82	7.06	UNK_AI173274	AI173274
112929_at	0.00	2.83	0.00	0.00	5.12	3.45	UNK_AA711463	AA711463
112988_at	0.00	0.00	0.00	3.10	5.72	4.74	UNK_AI006418	AI006418
113050_at	0.00	0.00	0.00	2.00	2.17	3.46	UNK_AI846034	AI846034
113122_i_at	0.00	2.46	0.73	2.33	3.55	0.00	UNK_AI843040	AI843040
113297_at	0.00	1.78	0.00	2.94	3.25	2.48	UNK_AW125352	AW125352
113335_at	0.00	0.00	0.00	3.40	7.49	12.56	UNK_AI876264	AI876264
113549_at	0.00	0.00	0.00	2.76	2.88	3.00	UNK_AI849286	AI849286
113622_at	0.00	0.00	1.78	2.89	3.75	7.10	UNK_AW046166	AW046166
113734_at	0.00	1.78	2.06	0.00	2.17	3.62	UNK_AA940541	AA940541
113743_at	0.00	0.00	0.00	3.40	3.14	3.99	UNK_AI854778	AI854778
113808_at	1.65	2.82	3.65	3.78	1.94	0.00	UNK_AA930477	AA930477
113914_at	0.00	0.00	0.00	3.60	4.87	4.90	UNK_AW121680	AW121680
113921_at	0.00	2.71	0.00	6.11	5.22	0.00	UNK_AW121531	AW121531
113931_at	0.00	0.00	0.00	5.86	20.80	7.34	UNK_AW230677	AW230677
113933_at	0.00	1.99	0.00	3.12	4.60	3.14	UNK_AI789270	AI789270
114091_at	0.00	4.16	4.06	2.47	1.71	0.00	UNK_AI450598	AI450598
114212_at	0.00	0.00	0.00	2.37	3.27	10.38	MRC2	AI430350
114240_at	0.00	0.00	0.00	2.57	3.20	3.35	UNK_AA816087	AA816087
114345_at	0.00	0.00	1.93	3.11	2.71	2.08	UNK_AI595956	AI595956
114362_at	1.85	0.00	4.86	4.77	2.19	0.00	UNK_AW208678	AW208678
114456_i_at	0.00	0.00	0.00	2.18	2.05	2.78	UNK_AI845540	AI845540
114457_f_at	0.00	0.00	0.00	2.03	2.05	2.60	UNK_AI845540	AI845540
114625_at	0.00	0.00	0.00	2.00	3.47	7.02	UNK_AI851509	AI851509
114639_at	0.00	1.75	0.00	3.14	6.05	5.01	UNK_AI317333	AI317333
114671_at	0.00	0.00	0.00	2.08	2.22	2.52	UNK_AI841352	AI841352
114704_at	0.00	0.00	0.00	3.00	2.86	3.76	UNK_AA822693	AA822693
114749_at	0.00	0.00	0.00	2.16	2.72	2.70	UNK_AW107659	AW107659
114807_at	0.00	0.00	2.23	2.33	1.46	2.09	UNK_AI627083	AI627083
114838_at	0.00	0.00	0.00	2.76	2.51	2.30	UNK_AA624264	AA624264
114850_at	0.00	4.93	20.51	5.87	0.00	0.00	UNK_AA138065	AA138065
115423_at	0.00	0.00	0.00	2.19	3.32	3.16	UNK_AW045388	AW045388
115489_at	0.00	1.75	1.96	2.11	2.67	3.02	UNK_AI851130	AI851130
115529_at	0.00	0.00	0.00	4.30	23.77	11.55	UNK_AI853798	AI853798
115530_at	0.00	0.00	2.66	0.00	4.19	2.70	UNK_AA034718	AA034718
115558_at	0.00	-1.22	0.00	5.43	15.06	4.67	UNK_AI549722	AI549722
115710_at	0.00	1.71	0.00	2.33	3.51	2.87	UNK_AW048553	AW048553
115782_at	0.00	0.00	0.00	2.58	3.24	2.25	UNK_AI845269	AI845269
115861_at	0.00	0.00	0.00	2.56	4.71	5.81	UNK_AA544955	AA544955
116019_at	0.00	0.00	0.00	2.31	4.51	4.20	UNK_AA646779	AA646779
116304_at	0.00	0.00	0.00	2.62	2.71	4.84	UNK_AI848982	AI848982
116342_at	0.00	0.00	1.99	2.40	2.04	2.09	UNK_AI605037	AI605037
116361_at	0.00	0.00	0.00	5.08	2.90	4.34	UNK_AW120661	AW120661
116371_at	0.00	1.76	2.58	1.92	2.39	2.10	UNK_AA184363	AA184363
116605_at	0.00	0.00	0.00	3.18	9.23	12.30	UNK_AI846130	AI846130
116807_at	0.00	0.00	0.00	2.83	8.66	13.74	UNK_AI846342	AI846342
116890_at	0.00	0.00	0.00	2.33	3.60	2.63	UNK_AW124225	AW124225
116956_at	0.00	0.00	0.00	3.64	7.36	6.60	UNK_AI848366	AI848366
116979_at	0.00	0.00	0.00	2.07	2.07	3.57	UNK_AW123277	AW123277
117071_at	0.00	0.00	0.00	2.46	6.44	10.77	UNK_AA796399	AA796399
117257_at	0.00	0.00	0.00	2.38	2.89	4.95	UNK_AI853746	AI853746
117317_at	0.00	0.00	0.00	5.30	7.21	4.70	UNK_AI851921	AI851921

128809_at	0.00	0.00	0.00	2.30	5.74	5.68	UNK_AA606775	AA606775
129315_at	0.00	0.00	0.00	2.13	2.07	2.28	UNK_AI122193	AI122193
129444_f_at	0.00	2.18	0.00	0.00	3.74	5.87	UNK_AW215481	AW215481
131513_s_at	0.00	0.00	0.00	2.13	2.35	5.06	UNK_AI415094	AI415094
134041_at	0.00	2.25	0.00	2.69	1.52	2.01	UNK_AA267733	AA267733
137130_at	0.00	0.00	0.00	3.26	3.04	4.23	UNK_AI662755	AI662755
92350_at	0.00	1.66	0.00	0.00	2.28	2.81	UNK_AA165759	AA165759
92778_i_at	0.00	0.00	0.00	0.00	2.57	2.94	virus locus 43; Mtv43	Z22552
92836_at	0.00	0.00	0.00	0.00	2.68	4.38	UNK_AA919594	AA919594
93376_at	0.00	2.10	2.01	0.00	1.58	1.62	0	AA673486
93437_f_at	0.00	0.00	1.17	0.00	2.71	3.32	UNK_AI850509	AI850509
93439_f_at	0.00	0.00	0.00	0.00	7.78	4.37	UNK_AA260005	AA260005
93440_at	0.00	0.00	0.00	0.00	2.55	2.36	0	AA692530
93480_at	0.00	0.00	0.00	1.72	3.43	2.21	UNK_AI845559	AI845559
93485_at	0.00	0.00	0.00	0.00	4.92	6.45	UNK_AI844911	AI844911
93496_at	0.00	0.00	0.00	1.93	2.03	2.48	UNK_AI852098	AI852098
93774_at	0.00	0.00	0.00	6.70	7.93	0.00	UNK_AW049040	AW049040
93835_at	0.00	0.00	0.00	0.00	3.31	3.09	UNK_AI843222	AI843222
94024_at	0.00	0.00	1.12	1.99	2.02	2.42	UNK_AA671429	AA671429
94081_at	0.00	0.00	0.00	3.48	2.65	0.00	UNK_AW124390	AW124390
94211_at	0.00	0.00	0.00	0.00	3.56	3.72	UNK_AA959180	AA959180
94332_at	0.00	0.00	0.00	0.00	2.04	2.61	UNK_AI882555	AI882555
94340_at	0.00	0.00	0.00	0.00	4.53	3.65	UNK_AW124224	AW124224
94374_at	0.00	0.00	0.00	2.30	1.99	2.48	UNK_AI850378	AI850378
94377_at	0.00	0.00	0.00	0.00	2.16	2.62	UNK_AI854793	AI854793
94395_at	0.00	0.00	0.00	1.91	2.23	3.23	UNK_AI194254	AI194254
94441_at	0.00	0.00	0.00	0.00	3.02	2.46	UNK_AW061237	AW061237
94506_at	0.00	0.00	2.59	0.00	2.93	1.86	UNK_AI853113	AI853113
94509_at	0.00	0.00	0.00	2.02	2.30	0.00	UNK_AI851207	AI851207
94548_at	0.00	1.28	1.48	2.07	1.86	2.36	UNK_AI790537	AI790537
94556_at	0.00	0.00	0.00	1.89	2.41	11.99	UNK_AI746846	AI746846
94689_at	0.00	0.00	0.00	0.00	2.23	2.86	UNK_C79248	C79248
94743_f_at	0.00	0.00	0.00	0.00	2.32	7.35	0	M29009
94814_at	0.00	1.90	1.70	0.00	3.26	3.29	UNK_AI957190	AI957190
94971_at	0.00	0.00	3.21	0.00	2.70	0.00	UNK_AI317217	AI317217
94989_at	0.00	0.00	0.00	2.00	2.33	2.29	UNK_AI848984	AI848984
94991_at	0.00	0.00	0.00	0.00	3.63	3.44	UNK_AW046661	AW046661
94993_f_at	0.00	0.00	0.00	0.00	2.61	11.61	UNK_M29010	M29010
95037_at	0.00	0.00	0.00	2.96	3.93	0.00	UNK_AW046639	AW046639
95118_r_at	0.00	0.00	0.00	0.00	5.66	4.58	UNK_AI131895	AI131895
95135_at	0.00	2.06	1.73	3.10	1.99	0.00	UNK_AI844396	AI844396
95150_at	0.00	2.53	0.00	2.86	1.48	1.58	UNK_AI852196	AI852196
95153_at	0.00	0.00	0.00	0.00	2.28	2.00	UNK_AI845988	AI845988
95288_i_at	0.00	0.00	0.00	1.42	2.84	2.83	0	AA189811
95387_f_at	0.00	0.00	0.00	0.00	3.38	2.85	0	AA266467
95420_at	0.00	0.00	0.00	0.00	2.57	3.47	UNK_AW120625	AW120625
95474_at	0.00	0.00	0.00	0.00	2.67	5.20	UNK_AW123850	AW123850
95496_at	0.00	0.00	0.00	0.00	4.46	3.06	UNK_AI848866	AI848866
95523_at	0.00	0.00	0.00	0.00	2.13	2.82	UNK_AI839718	AI839718
95593_at	0.00	0.00	0.00	1.98	5.35	4.42	UNK_AW125446	AW125446
95612_at	0.00	1.74	3.56	0.00	3.63	0.00	UNK_AA667128	AA667128
95656_i_at	0.00	2.27	2.14	0.00	0.00	0.00	D13WSU177E	AW125164
95677_at	0.00	0.00	0.00	0.00	2.40	2.21	UNK_AA881621	AA881621
95723_r_at	0.00	0.00	0.00	1.53	2.04	2.07	SUPT6H	AI841464
95732_at	0.00	0.00	0.00	2.19	2.49	0.00	UNK_AW047746	AW047746
95881_f_at	0.00	0.00	0.00	0.00	3.08	2.41	UNK_AI447783	AI447783
96132_at	0.00	0.00	1.29	0.00	3.66	4.28	UNK_AB023957	AB023957
96154_at	0.00	0.00	0.00	3.17	1.96	4.47	UNK_AA600645	AA600645

96200_at	0.00	1.80	0.00	2.95	5.39	0.00	UNK_AI838344	AI838344
96236_at	0.00	0.00	0.00	2.36	3.17	1.99	UNK_AW122965	AW122965
96264_at	0.00	0.00	0.00	2.56	4.65	0.00	UNK_AW061235	AW061235
96266_at	0.00	0.00	1.86	2.85	2.40	1.74	UNK_AI841982	AI841982
96272_at	0.00	0.00	0.00	0.00	4.76	4.20	UNK_AI848471	AI848471
96336_at	0.00	1.53	0.00	2.46	2.17	0.00	UNK_AI844626	AI844626
96360_at	0.00	1.65	0.00	0.00	3.16	3.53	UNK_AW125498	AW125498
96464_at	0.00	0.00	0.00	1.94	2.50	2.50	0	N28179
96602_g_at	0.00	0.00	0.00	0.00	4.91	4.54	UNK_AW045751	AW045751
96716_at	0.00	0.00	0.00	0.00	2.39	2.46	UNK_AW121102	AW121102
96818_at	0.00	0.00	0.00	0.00	2.72	2.98	UNK_AA762522	AA762522
96832_at	0.00	0.00	0.00	2.05	1.96	2.56	UNK_AA606878	AA606878
96896_at	0.00	1.77	0.00	2.42	1.85	2.35	UNK_AW214159	AW214159
96924_at	0.00	0.00	0.00	0.00	2.43	2.83	UNK_AI849719	AI849719
96925_at	0.00	0.00	0.00	3.83	4.12	1.93	UNK_AW122429	AW122429
97163_g_at	0.00	0.00	0.00	0.00	2.04	3.16	UNK_AI563699	AI563699
97269_f_at	0.00	0.00	0.00	2.11	2.23	1.88	UNK_AI848699	AI848699
97311_at	0.00	0.00	0.00	2.11	2.02	1.97	UNK_AI836509	AI836509
97329_at	0.00	0.00	0.00	0.00	2.18	2.05	UNK_AW124061	AW124061
97349_at	0.00	0.00	0.00	0.00	3.35	5.09	UNK_AA727410	AA727410
97398_at	0.00	0.00	0.00	0.00	6.60	6.60	UNK_AI849831	AI849831
97451_at	0.00	2.12	0.00	2.88	1.85	1.82	UNK_AI837599	AI837599
97560_at	0.00	0.00	0.00	0.00	2.40	2.30	UNK_AF037437	AF037437
97809_at	0.00	0.00	0.00	1.83	2.19	2.27	UNK_AF109906	AF109906
97919_at	0.00	0.00	0.00	0.00	2.28	2.08	UNK_AI837467	AI837467
98060_at	0.00	0.00	2.93	0.00	4.09	0.00	lamin A; Lmna	D49733
98355_at	0.00	0.00	0.00	0.00	2.92	6.08	0	AA544993
98492_at	0.00	1.34	0.00	0.00	2.63	2.76	UNK_AA920419	AA920419
98515_at	0.00	1.85	0.00	0.00	3.10	2.80	UNK_AI844392	AI844392
98633_at	0.00	0.00	0.00	2.17	2.06	1.93	UNK_AI854863	AI854863
99156_at	0.00	0.00	0.00	0.00	2.24	2.28	UNK_AI853370	AI853370
99163_at	0.00	0.00	0.00	0.00	6.28	3.78	UNK_AI844232	AI844232
99168_at	0.00	0.00	0.00	0.00	3.58	3.28	UNK_AW047128	AW047128
99338_at	0.00	0.00	0.00	0.00	4.39	4.16	UNK_AA674798	AA674798
99451_at	0.00	0.00	0.00	0.00	12.07	9.19	UNK_AW060510	AW060510
99467_at	0.00	0.00	0.00	0.00	2.01	2.13	UNK_AI846922	AI846922
99645_at	0.00	0.00	0.00	0.00	2.10	3.75	UNK_AW048484	AW048484
99992_at	0.00	2.80	0.00	0.00	2.29	0.00	IL17R	AI286698
100466_f_at	0.00	0.00	0.00	0.00	3.15	4.34	UNK_AA655823	AA655823
100979_at	0.00	0.00	0.00	0.00	2.36	3.04	UNK_AW209763	AW209763
100988_at	0.00	0.00	0.00	0.00	2.12	4.41	UNK_AA796690	AA796690
101426_at	0.00	0.00	0.00	0.00	3.70	4.09	UNK_AW125333	AW125333
101432_at	0.00	0.00	0.00	0.00	3.51	3.76	UNK_AI504100	AI504100
101505_at	0.00	0.00	0.00	0.00	3.05	2.74	UNK_AW121234	AW121234
101851_at	0.00	0.00	0.00	0.00	3.98	4.82	MOX2	AF029215
101882_s_at	0.00	0.00	0.00	0.00	6.36	2.59	procollagen, type XV,procollagen, type XVIII, alpha 1; Col15a1,Col18a1	U03715
102099_f_at	0.00	0.00	0.00	1.68	5.10	3.69	UNK_AI843637	AI843637
102331_at	0.00	0.00	0.00	2.40	2.51	0.00	UNK_AW120586	AW120586
102352_at	0.00	0.00	0.00	0.00	6.99	3.33	UNK_AW121380	AW121380
102370_at	0.00	0.00	0.00	2.09	1.71	4.73	UNK_AA822174	AA822174
102562_at	0.00	0.00	0.00	0.00	2.02	2.12	UNK_Z80833	Z80833
102848_f_at	0.00	0.00	0.00	0.00	8.43	5.42	UNK_AI840577	AI840577
102942_at	0.00	0.00	0.00	0.00	2.12	4.85	UNK_AA683785	AA683785
103082_at	0.00	0.00	1.69	1.90	2.78	3.55	UNK_AI847507	AI847507
103100_at	0.00	0.00	0.00	0.00	3.42	2.16	UNK_AI788543	AI788543
103218_at	0.00	0.00	1.24	0.00	2.76	4.58	0	J04761

103260_at	0.00	1.71	0.00	2.55	1.53	5.42	UNK_AI838553	AI838553
103400_at	0.00	0.00	0.00	1.70	2.18	2.55	Unknown	D50523
103402_at	0.00	0.00	0.00	0.00	3.66	4.38	UNK_AI848522	AI848522
103415_at	0.00	0.00	0.00	0.00	2.85	2.49	UNK_AI840925	AI840925
103459_at	0.00	1.44	0.00	0.00	3.28	2.82	UNK_AW124544	AW124544
103460_at	0.00	0.00	0.00	0.00	8.28	9.43	UNK_AI849939	AI849939
103462_at	0.00	2.50	2.95	0.00	1.56	1.78	UNK_AW122239	AW122239
103529_at	0.00	0.00	0.00	0.00	3.16	3.32	UNK_AW125505	AW125505
103545_at	0.00	0.00	1.85	2.19	2.94	1.98	UNK_AA240695	AA240695
103631_at	0.00	0.00	0.00	2.14	2.17	0.00	UNK_AA985795	AA985795
103635_at	0.00	0.00	0.00	0.00	2.73	2.60	UNK_AI648925	AI648925
103643_at	0.00	0.00	0.00	2.11	2.07	0.00	UNK_AI844784	AI844784
103717_at	0.00	0.00	0.00	2.44	4.25	0.00	UNK_AA921411	AA921411
103736_at	0.00	0.00	1.88	2.30	1.99	3.39	UNK_AI837786	AI837786
103752_r_at	0.00	0.00	0.00	0.00	2.43	2.39	UNK_AW227545	AW227545
103891_i_at	0.00	0.00	0.00	0.00	3.19	2.98	UNK_AI197161	AI197161
103892_r_at	0.00	0.00	0.00	0.00	3.23	3.91	UNK_AI197161	AI197161
103932_at	0.00	1.87	0.00	2.20	2.21	1.71	UNK_AA655311	AA655311
103989_at	0.00	0.00	0.00	1.71	2.99	2.62	UNK_AI314715	AI314715
104002_at	0.00	0.00	0.00	0.00	4.37	2.28	UNK_AI153693	AI153693
104004_at	0.00	0.00	0.00	0.00	3.04	4.20	UNK_AI931876	AI931876
104065_at	0.00	1.42	1.95	0.00	2.82	3.61	UNK_AW212878	AW212878
104105_at	0.00	0.00	0.00	0.00	3.30	3.23	UNK_AI854665	AI854665
104119_at	0.00	0.00	0.00	0.00	2.19	3.50	UNK_AI845028	AI845028
104306_at	0.00	0.00	0.00	3.41	3.36	0.00	UNK_AI847886	AI847886
104350_at	0.00	0.00	0.00	0.00	2.43	3.37	UNK_AI050321	AI050321
104412_at	0.00	0.00	0.00	0.00	3.91	5.94	UNK_AI153412	AI153412
104559_at	0.00	0.00	0.00	0.00	2.03	2.13	UNK_AI848162	AI848162
104573_at	0.00	1.68	0.00	2.24	2.03	0.00	UNK_AA921069	AA921069
104576_at	0.00	0.00	0.00	2.05	1.69	2.10	[H.SAPIENS]	AW212397
104620_at	0.00	0.00	0.00	0.00	3.31	2.61	UNK_AW123402	AW123402
104697_at	0.00	0.00	0.00	0.00	2.23	2.13	UNK_AW121127	AW121127
104761_at	0.00	0.00	0.00	0.00	2.03	3.75	UNK_AA612450	AA612450
104932_at	0.00	0.00	0.00	1.83	4.86	3.78	UNK_AA197852	AA197852
104948_at	0.00	0.00	0.00	0.00	2.26	2.71	UNK_AI591666	AI591666
104983_at	0.00	0.00	0.00	1.68	4.08	2.97	UNK_AA611753	AA611753
105012_at	0.00	0.00	0.00	1.94	3.33	2.51	UNK_AI225316	AI225316
105453_at	0.00	0.00	0.00	0.00	2.88	6.18	UNK_AI606622	AI606622
105500_at	0.00	0.00	0.00	1.94	3.03	7.55	UNK_AA389264	AA389264
105538_at	0.00	0.00	0.00	0.00	2.54	3.39	UNK_AA125182	AA125182
105580_at	0.00	0.00	0.00	0.00	2.51	2.56	UNK_AA517795	AA517795
105647_at	0.00	0.00	0.00	0.00	7.93	3.57	UNK_AI785246	AI785246
105659_f_at	0.00	0.00	0.00	1.50	2.02	2.83	UNK_AI789447	AI789447
105797_at	0.00	2.70	0.00	2.84	0.00	0.00	UNK_AI842817	AI842817
105858_at	0.00	1.49	1.76	3.05	5.07	0.00	UNK_AI847445	AI847445
105859_at	0.00	0.00	0.00	0.00	2.11	3.34	UNK_AI834985	AI834985
105893_at	0.00	0.00	0.00	0.00	2.08	2.51	UNK_AI852905	AI852905
106033_at	0.00	0.00	0.00	1.47	2.68	2.69	UNK_AW125624	AW125624
106046_at	0.00	0.00	0.00	1.57	3.54	2.03	UNK_AI847176	AI847176
106072_at	0.00	0.00	0.00	2.01	2.17	0.00	UNK_AW122135	AW122135
106085_at	0.00	0.00	0.00	0.00	2.40	2.34	UNK_AI850834	AI850834
106150_at	0.00	0.00	0.00	0.00	3.81	6.45	UNK_AI840953	AI840953
106152_at	0.00	0.00	0.00	0.00	3.62	4.07	UNK_AI845991	AI845991
106153_g_at	0.00	0.00	0.00	1.63	2.98	3.81	UNK_AI845991	AI845991
106195_at	0.00	-1.73	0.00	0.00	4.88	2.93	UNK_AI851948	AI851948
106196_at	0.00	0.00	0.00	0.00	3.65	3.47	UNK_AW060432	AW060432
106237_at	0.00	0.00	0.00	0.00	3.40	3.75	UNK_AI841243	AI841243
106256_at	0.00	1.29	2.14	1.85	2.23	1.17	UNK_AA624068	AA624068
106274_at	0.00	0.00	0.00	2.03	1.90	2.61	UNK_AI835482	AI835482

106280_at	0.00	0.00	0.00	0.00	2.19	2.21	UNK_AW124976	AW124976
106508_at	0.00	0.00	0.00	0.00	2.37	2.30	UNK_AA833228	AA833228
106568_at	0.00	0.00	0.00	0.00	2.62	2.80	UNK_AW121589	AW121589
106575_at	0.00	0.00	0.00	0.00	2.21	2.02	UNK_AI837294	AI837294
106593_g_at	0.00	0.00	0.00	0.00	3.66	2.41	UNK_AI115629	AI115629
106602_at	0.00	3.16	0.00	0.00	3.00	0.00	UNK_AA638815	AA638815
106892_at	0.00	0.00	0.00	0.00	3.46	5.31	UNK_AW124490	AW124490
106927_at	0.00	0.00	0.00	0.00	3.65	3.89	UNK_AI882582	AI882582
106930_at	0.00	0.00	0.00	1.93	5.20	2.02	UNK_AW123721	AW123721
106941_at	0.00	0.00	0.00	2.08	1.82	2.75	UNK_AA839645	AA839645
106997_at	0.00	0.00	0.00	2.35	1.77	2.72	UNK_AI463148	AI463148
107009_at	0.00	0.00	0.00	0.00	7.44	2.74	UNK_AI842805	AI842805
107042_at	0.00	0.00	0.00	0.00	2.60	3.78	UNK_AW045813	AW045813
107112_at	0.00	0.00	0.00	0.00	3.76	10.09	UNK_AI121797	AI121797
107378_at	0.00	0.00	0.00	0.00	2.15	3.49	UNK_AW050170	AW050170
107399_at	0.00	0.00	0.00	0.00	2.49	6.12	UNK_AW060961	AW060961
107423_at	0.00	0.00	0.00	0.00	2.48	2.26	UNK_AI852884	AI852884
107438_at	0.00	0.00	0.00	0.00	3.20	4.12	UNK_AI838142	AI838142
107518_at	0.00	0.00	0.00	0.00	2.38	2.62	UNK_AA832766	AA832766
107581_at	0.00	0.00	0.00	2.32	2.35	0.00	UNK_AI843686	AI843686
107596_at	0.00	0.00	0.00	-1.14	9.07	4.95	UNK_AW125675	AW125675
107598_at	0.00	0.00	0.00	1.92	5.33	5.65	UNK_AW047810	AW047810
107830_at	0.00	0.00	0.00	0.00	3.29	4.02	UNK_AI390404	AI390404
107916_at	0.00	0.00	0.00	0.00	2.76	2.66	UNK_AA790833	AA790833
107994_at	0.00	0.00	0.00	1.31	3.83	6.08	UNK_AI842351	AI842351
108014_at	0.00	0.00	0.00	0.00	2.07	3.81	UNK_AI551155	AI551155
108330_at	0.00	0.00	0.00	0.00	2.71	4.28	UNK_AI197423	AI197423
108339_at	0.00	0.00	0.00	0.00	2.25	2.80	UNK_AI552478	AI552478
108365_at	0.00	0.00	0.00	2.22	2.71	0.00	UNK_AA981778	AA981778
108367_at	0.00	0.00	0.00	1.62	2.34	2.24	UNK_AI842852	AI842852
108478_f_at	0.00	0.00	0.00	0.00	4.66	11.84	UNK_AI785264	AI785264
108504_at	0.00	0.00	0.00	0.00	2.43	3.32	UNK_AA795013	AA795013
108565_at	0.00	-2.68	-2.95	0.00	2.66	4.55	UNK_AI853095	AI853095
108575_at	0.00	0.00	0.00	0.00	3.01	2.34	UNK_AI842010	AI842010
108734_at	0.00	0.00	0.00	0.00	4.10	8.50	UNK_AI853716	AI853716
108783_at	0.00	0.00	0.00	0.00	6.00	11.46	UNK_AI835933	AI835933
108784_at	0.00	0.00	0.00	0.00	8.87	8.96	UNK_AI427138	AI427138
108811_at	0.00	1.85	2.48	2.14	0.00	0.00	UNK_AA981032	AA981032
108969_at	0.00	0.00	0.00	0.00	3.24	2.99	UNK_AA220091	AA220091
108973_at	0.00	0.00	0.00	0.00	2.39	2.49	UNK_AA958878	AA958878
109013_at	0.00	0.00	0.00	0.00	2.37	4.57	UNK_AA710128	AA710128
109040_at	0.00	0.00	0.00	0.00	3.68	2.21	UNK_AW213256	AW213256
109104_at	0.00	0.00	0.00	0.00	2.21	2.65	UNK_AI853670	AI853670
109114_at	0.00	0.00	0.00	2.29	2.25	0.00	UNK_AA792643	AA792643
109123_at	0.00	0.00	0.00	0.00	5.75	10.65	UNK_AI839366	AI839366
109135_at	0.00	0.00	0.00	0.00	4.42	3.77	UNK_AA645519	AA645519
109144_at	0.00	0.00	0.00	0.00	6.29	4.92	UNK_AI852146	AI852146
109163_f_at	0.00	0.00	0.00	0.00	4.48	3.62	UNK_AI847246	AI847246
109164_r_at	0.00	0.00	0.00	1.81	2.47	3.32	UNK_AI847246	AI847246
109177_at	0.00	0.00	0.00	4.70	6.77	0.00	UNK_AW122327	AW122327
109184_at	0.00	1.79	0.00	0.00	2.84	2.26	UNK_AI036137	AI036137
109337_at	0.00	0.00	0.00	0.00	2.29	2.89	UNK_AW215538	AW215538
109341_at	0.00	0.00	0.00	0.00	2.59	4.05	UNK_AW124078	AW124078
109358_f_at	0.00	0.00	0.00	1.22	3.44	4.46	UNK_AI854068	AI854068
109359_r_at	0.00	-1.18	0.00	0.00	2.84	3.91	UNK_AI854068	AI854068
109385_at	0.00	0.00	4.32	3.49	0.00	0.00	UNK_AI315194	AI315194
109490_at	0.00	0.00	0.00	0.00	3.14	8.37	UNK_AI646305	AI646305
109622_at	0.00	0.00	0.00	0.00	7.24	4.22	UNK_AI594717	AI594717
109643_at	0.00	0.00	0.00	0.00	4.67	4.71	UNK_AA170471	AA170471

109689_at	0.00	0.00	0.00	0.00	2.74	4.09	UNK_AI115717	AI115717
109739_at	0.00	2.73	0.00	0.00	4.00	0.00	UNK_AI853736	AI853736
109744_at	0.00	2.54	0.00	4.22	0.00	0.00	UNK_AW046698	AW046698
109749_at	0.00	0.00	0.00	1.65	2.85	5.82	UNK_AW125440	AW125440
109762_at	0.00	0.00	0.00	0.00	4.69	2.51	UNK_AI854227	AI854227
109775_at	0.00	0.00	0.00	2.41	4.00	0.00	UNK_AI842966	AI842966
109776_at	0.00	0.00	0.00	1.93	2.82	3.21	UNK_AI849150	AI849150
109824_f_at	0.00	0.00	1.81	2.63	1.78	2.24	UNK_AI835703	AI835703
109911_at	0.00	0.00	0.00	1.78	2.49	2.74	UNK_AW107484	AW107484
110076_at	0.00	0.00	0.00	0.00	2.82	3.16	UNK_AI646560	AI646560
110107_at	0.00	0.00	0.00	0.00	2.36	2.13	UNK_AI036500	AI036500
110145_at	0.00	0.00	0.00	0.00	2.50	2.23	UNK_AW061334	AW061334
110147_at	0.00	0.00	0.00	0.00	2.43	2.54	UNK_AW227605	AW227605
110181_at	0.00	2.33	0.00	0.00	1.85	3.45	UNK_AW123683	AW123683
110229_at	0.00	5.00	3.44	1.99	0.00	0.00	UNK_AA959125	AA959125
110259_at	0.00	0.00	0.00	0.00	2.31	3.82	UNK_AA057986	AA057986
110262_at	0.00	0.00	0.00	-1.18	2.16	3.05	UNK_AI154379	AI154379
110295_at	0.00	0.00	0.00	0.00	2.84	10.26	UNK_AW046707	AW046707
110322_at	0.00	0.00	0.00	1.21	2.91	2.45	UNK_AI846841	AI846841
110324_at	0.00	0.00	0.00	0.00	3.04	2.32	UNK_AI155963	AI155963
110328_at	0.00	0.00	0.00	0.00	3.87	2.83	UNK_AI842437	AI842437
110329_at	0.00	0.00	0.00	2.01	1.72	2.38	UNK_AI430629	AI430629
110372_at	0.00	0.00	1.88	2.66	2.07	0.00	UNK_AI834822	AI834822
110435_at	0.00	0.00	0.00	0.00	2.57	2.67	UNK_AI851412	AI851412
110437_at	0.00	0.00	0.00	2.01	3.19	0.00	UNK_AW108175	AW108175
110443_at	0.00	0.00	0.00	0.09	3.58	3.70	UNK_AW123547	AW123547
110585_at	0.00	0.00	0.00	0.00	2.40	2.22	UNK_AA221341	AA221341
110591_at	0.00	0.00	0.00	0.00	3.39	4.94	UNK_AA270831	AA270831
110632_at	0.00	0.00	0.00	1.79	2.14	3.87	UNK_AI021658	AI021658
110634_at	0.00	0.00	0.00	0.00	2.32	2.37	UNK_AA644787	AA644787
110732_at	0.00	0.00	0.00	0.00	2.42	2.39	UNK_AA763948	AA763948
110738_at	0.00	0.00	0.00	1.87	2.37	2.59	UNK_AA867029	AA867029
110743_at	0.00	0.00	0.00	0.00	4.96	6.38	UNK_AW121291	AW121291
110810_at	0.00	0.00	0.00	2.02	1.67	2.82	UNK_AI844703	AI844703
111072_at	0.00	0.00	0.00	1.36	2.20	2.36	UNK_AA739282	AA739282
111080_at	0.00	0.00	0.00	0.00	2.24	3.71	UNK_AA762313	AA762313
111124_at	0.00	0.00	0.00	1.48	3.16	3.45	UNK_AA472921	AA472921
111209_at	0.00	0.00	0.00	3.55	2.55	0.00	UNK_AW122433	AW122433
111336_at	0.00	0.00	0.00	0.00	19.09	8.17	UNK_AI841087	AI841087
111358_at	0.00	0.00	0.00	0.00	2.87	4.47	UNK_AI785284	AI785284
111383_at	0.00	0.00	0.00	0.00	2.10	2.13	UNK_AI848661	AI848661
111412_at	0.00	0.00	0.00	0.00	4.68	11.73	UNK_AW123189	AW123189
111429_f_at	0.00	0.00	0.00	0.00	3.32	3.05	UNK_AW011836	AW011836
111447_at	0.00	0.00	0.00	2.15	1.70	2.18	UNK_AI837588	AI837588
111476_at	0.00	0.00	0.00	0.00	4.26	5.02	UNK_AW045512	AW045512
111695_at	0.00	0.00	0.00	2.23	4.07	0.00	UNK_AW125745	AW125745
111698_at	0.00	0.00	0.00	0.00	2.31	2.74	UNK_AW121218	AW121218
111735_at	0.00	0.00	0.00	2.98	1.45	2.74	UNK_AI061010	AI061010
111747_at	0.00	0.00	0.00	0.00	2.44	2.94	UNK_AW215531	AW215531
111809_r_at	0.00	0.00	0.00	0.00	6.07	5.28	UNK_AW049301	AW049301
111820_at	0.00	0.00	0.00	0.00	2.28	2.14	UNK_AI225827	AI225827
111842_at	0.00	0.00	0.00	0.00	2.39	2.76	UNK_AW121081	AW121081
111887_at	0.00	0.00	0.00	0.00	2.19	2.38	UNK_AA726802	AA726802
111975_at	0.00	0.00	0.00	0.00	6.01	5.95	UNK_AI844650	AI844650
111998_at	0.00	0.00	0.00	0.00	2.61	2.22	UNK_AI606832	AI606832
112002_at	0.00	0.00	0.00	0.00	4.22	2.88	UNK_AI641819	AI641819
112019_at	0.00	0.00	0.00	0.00	3.76	4.45	UNK_AA881092	AA881092
112245_at	0.00	0.00	0.00	0.00	4.57	5.35	UNK_AW122302	AW122302
112257_at	0.00	0.00	0.00	1.84	2.97	6.53	UNK_AA958476	AA958476

112284_at	0.00	0.00	0.00	0.00	3.54	8.72	UNK_AW124683	AW124683
112288_at	0.00	0.00	0.00	0.00	8.31	6.31	UNK_AW120568	AW120568
112289_g_at	0.00	0.00	0.00	1.34	3.02	3.48	UNK_AW120568	AW120568
112337_at	0.00	0.00	0.00	0.00	2.56	2.03	UNK_AW045621	AW045621
112355_at	0.00	0.00	0.00	0.00	2.23	2.45	UNK_AI156083	AI156083
112358_at	0.00	0.00	0.00	0.00	2.24	4.50	UNK_AA681243	AA681243
112374_at	0.00	0.00	0.00	5.63	2.94	0.00	UNK_AW046652	AW046652
112378_at	0.00	0.00	0.00	2.04	1.86	2.06	UNK_AI842868	AI842868
112431_at	0.00	0.00	0.00	1.58	2.09	2.91	UNK_AI853946	AI853946
112472_at	0.00	0.00	0.00	0.00	2.38	3.08	UNK_AI286746	AI286746
112482_at	0.00	0.00	0.00	1.29	2.05	2.04	UNK_AW208789	AW208789
112704_at	0.00	0.00	0.00	1.67	2.06	2.33	UNK_AW228808	AW228808
112706_at	0.00	0.00	0.00	1.69	6.43	5.73	UNK_AW212497	AW212497
112718_at	0.00	1.41	0.00	2.02	2.27	0.00	UNK_AW230461	AW230461
112743_at	0.00	0.00	0.00	0.00	2.31	2.41	UNK_AI157595	AI157595
112747_at	0.00	1.77	1.64	2.12	1.86	2.04	UNK_AW106365	AW106365
112768_at	0.00	0.00	0.00	0.00	2.01	2.45	UNK_AI227355	AI227355
112792_at	1.77	1.62	0.00	2.00	1.83	2.40	UNK_AI843762	AI843762
112794_at	0.00	0.00	0.00	0.00	2.12	4.37	UNK_AI844497	AI844497
112877_at	0.00	0.00	0.00	0.00	9.13	6.99	UNK_AW228014	AW228014
112892_at	0.00	0.00	0.00	0.00	3.90	2.90	UNK_AI316340	AI316340
112911_r_at	0.00	0.00	0.00	1.98	7.48	2.42	UNK_AW229261	AW229261
112924_at	0.00	0.00	0.00	0.00	2.19	3.79	UNK_AI842606	AI842606
112934_at	0.00	0.00	0.00	1.94	5.22	4.57	UNK_AI845672	AI845672
112943_at	0.00	0.00	0.00	1.58	2.45	2.73	UNK_AI462057	AI462057
112955_at	0.00	0.00	0.00	0.00	26.37	10.55	UNK_AW122703	AW122703
112993_at	0.00	0.00	0.00	0.00	4.43	2.63	UNK_AA798461	AA798461
113033_at	0.00	0.00	0.00	2.25	1.72	2.00	UNK_AW049519	AW049519
113048_at	0.00	0.00	0.00	1.46	2.11	3.42	UNK_AA717403	AA717403
113114_at	0.00	0.00	0.00	0.00	8.30	7.15	UNK_AI842299	AI842299
113142_at	0.00	1.46	0.00	1.82	4.37	4.99	UNK_AI854696	AI854696
113145_at	0.00	0.00	0.00	0.00	2.61	3.12	UNK_AI838163	AI838163
113198_at	0.00	0.00	1.66	2.26	2.60	0.00	UNK_AI851615	AI851615
113250_at	0.00	0.00	0.00	0.00	2.13	2.69	UNK_AI847212	AI847212
113286_at	0.00	0.00	0.00	2.66	1.54	2.22	UNK_AI845147	AI845147
113442_at	0.00	0.00	2.13	2.10	1.47	0.00	UNK_AI613741	AI613741
113495_at	0.00	0.00	0.00	0.00	2.21	3.10	UNK_AI595304	AI595304
113575_at	0.00	0.00	0.00	2.14	3.04	0.00	UNK_AI931943	AI931943
113590_at	0.00	0.00	0.00	0.00	2.10	2.13	UNK_AI931548	AI931548
113640_at	0.00	0.00	0.00	0.00	13.54	17.72	UNK_AW045201	AW045201
113650_at	0.00	0.00	0.00	0.00	8.85	9.09	UNK_AW049728	AW049728
113674_at	0.00	0.00	1.00	0.00	3.44	3.04	UNK_AI505611	AI505611
113692_at	0.00	0.00	0.00	1.90	2.09	3.43	UNK_AA666755	AA666755
113749_at	0.00	0.00	0.00	0.00	2.85	3.63	UNK_AA960059	AA960059
113766_at	0.00	0.00	0.00	0.00	2.74	3.34	UNK_AI854004	AI854004
113851_at	0.00	0.00	0.00	0.00	3.25	5.14	UNK_AA204063	AA204063
113912_at	0.00	0.00	0.00	0.00	2.91	4.00	UNK_AW123902	AW123902
113926_at	0.00	0.00	0.00	0.00	2.31	2.82	UNK_AW228609	AW228609
113970_at	0.00	0.00	0.00	1.16	2.89	2.02	UNK_AW229038	AW229038
114199_at	0.00	0.00	0.00	1.61	4.96	4.23	UNK_AA215054	AA215054
114224_at	0.00	0.00	0.00	0.00	8.65	10.01	UNK_AI425989	AI425989
114254_at	0.00	0.00	0.00	0.00	3.94	2.14	UNK_AA183037	AA183037
114271_at	0.00	0.00	0.00	0.00	3.02	2.28	UNK_AA794755	AA794755
114420_at	0.00	-3.91	-3.29	0.00	3.25	4.37	UNK_AA734866	AA734866
114426_at	0.00	0.00	0.00	0.00	3.18	3.42	UNK_AI480529	AI480529
114468_at	0.00	0.00	0.00	0.00	3.35	2.89	UNK_AI845124	AI845124
114475_at	0.00	0.00	0.00	0.00	2.43	2.28	UNK_AI839459	AI839459
114483_at	0.00	0.00	0.00	0.00	3.83	4.62	UNK_AW122384	AW122384
114562_at	0.00	-1.08	0.00	0.00	6.04	7.48	UNK_AA710515	AA710515

114589_at	0.00	0.00	0.00	1.96	2.17	3.62	UNK_AA792890	AA792890
114689_at	0.00	0.00	0.00	2.80	3.79	0.00	UNK_AW045811	AW045811
114694_at	0.00	0.00	0.00	0.00	2.21	2.96	UNK_AI848139	AI848139
114750_at	0.00	0.00	1.76	1.57	2.37	2.13	UNK_AW046379	AW046379
114774_at	0.00	0.00	0.00	0.00	2.22	3.98	TCF7L2	AW211815
114790_at	0.00	0.00	0.00	0.00	2.64	3.20	UNK_AI594026	AI594026
114791_at	0.00	0.00	0.00	0.00	3.14	4.04	UNK_AI834978	AI834978
114795_at	0.00	0.00	0.00	0.00	2.26	2.83	UNK_AI158227	AI158227
114815_at	0.00	0.00	0.00	0.00	3.31	2.88	UNK_AI155547	AI155547
114857_at	0.00	0.00	0.00	2.87	3.49	0.00	UNK_AW048104	AW048104
114994_at	0.00	0.00	0.00	0.00	2.80	2.87	UNK_AW050047	AW050047
115028_at	0.00	0.00	0.00	0.09	2.64	6.54	UNK_AA711308	AA711308
115033_f_at	0.00	0.00	0.00	2.17	3.65	0.00	UNK_AI848847	AI848847
115107_at	0.00	0.00	0.00	1.26	17.16	2.58	UNK_AW125312	AW125312
115116_at	1.39	0.00	0.00	0.00	2.02	2.17	UNK_AW121890	AW121890
115145_at	0.00	0.00	0.00	2.13	2.14	0.00	UNK_AA789611	AA789611
115185_at	0.00	0.00	0.00	2.52	3.20	0.00	UNK_AW124312	AW124312
115200_at	0.00	0.00	0.00	0.00	3.56	2.19	UNK_AI643806	AI643806
115210_at	0.00	0.00	0.00	0.00	7.58	2.25	UNK_AA985762	AA985762
115219_at	0.00	0.00	0.00	0.00	5.64	5.93	UNK_AI607010	AI607010
115315_at	0.00	0.00	0.00	0.00	2.12	2.43	UNK_AA068501	AA068501
115361_at	0.00	0.00	0.00	1.31	2.33	2.22	UNK_AU045961	AU045961
115543_at	0.00	0.00	0.00	0.00	2.32	2.45	UNK_AW120607	AW120607
115570_f_at	0.00	0.00	0.00	1.83	2.15	3.21	UNK_AI428995	AI428995
115776_at	0.00	0.00	0.00	0.00	3.11	2.09	UNK_AI132212	AI132212
115811_at	0.00	0.00	0.00	0.00	16.04	6.53	UNK_AA795075	AA795075
115820_at	0.00	0.00	0.00	0.00	2.27	4.56	UNK_AI852255	AI852255
115859_at	0.00	0.00	0.00	2.76	6.40	0.00	UNK_AI159157	AI159157
115926_at	0.00	0.00	0.00	0.00	21.98	21.56	UNK_AA839289	AA839289
115932_at	0.00	0.00	0.00	0.00	3.54	3.31	UNK_AW047504	AW047504
115956_at	0.00	0.00	0.00	1.73	2.39	4.92	UNK_AA472455	AA472455
115962_at	0.00	0.00	0.00	0.00	14.87	7.81	UNK_AI615325	AI615325
116031_at	0.00	0.00	0.00	0.00	2.05	2.39	UNK_AI843837	AI843837
116072_at	0.00	0.00	0.00	2.47	2.74	0.00	UNK_AI853043	AI853043
116124_at	0.00	0.00	0.00	0.00	2.83	3.36	UNK_AI466198	AI466198
116132_at	0.00	0.00	0.00	2.75	3.17	0.00	UNK_AI851807	AI851807
116197_at	0.00	0.00	0.00	2.33	2.24	0.00	UNK_AI132005	AI132005
116253_at	0.00	0.00	0.00	0.00	2.67	3.74	UNK_AI843499	AI843499
116303_at	0.00	0.00	0.00	1.58	3.25	2.23	UNK_AA592780	AA592780
116432_at	0.00	0.00	0.00	1.91	4.84	3.49	UNK_AI845744	AI845744
116470_at	0.00	0.00	0.00	0.00	2.21	4.31	UNK_AW047556	AW047556
116594_at	0.00	0.00	0.00	1.94	5.23	4.43	UNK_AW047008	AW047008
116600_at	0.51	0.00	0.00	0.00	6.42	2.37	UNK_AI848448	AI848448
116612_at	0.00	0.00	0.00	0.00	3.08	3.73	UNK_AI854230	AI854230
116627_at	0.00	0.00	0.00	0.00	2.11	2.05	UNK_AI608135	AI608135
116659_at	0.00	0.00	0.00	0.00	2.73	3.51	UNK_AI854578	AI854578
116678_at	0.00	0.00	0.00	2.39	2.23	1.68	UNK_AI256490	AI256490
116719_at	0.00	0.00	1.74	2.05	1.88	2.31	UNK_AI850429	AI850429
116806_at	0.00	-0.05	1.09	0.64	12.02	5.79	UNK_AI481202	AI481202
116809_at	0.00	0.00	0.00	0.00	3.34	4.18	UNK_AW120749	AW120749
116823_at	0.00	0.00	0.00	0.00	2.68	3.08	UNK_AI314071	AI314071
116837_at	0.00	0.00	0.00	0.00	3.43	3.94	UNK_AI839054	AI839054
116860_at	0.00	0.00	0.00	0.00	2.22	2.51	UNK_AA929441	AA929441
116908_at	0.00	0.00	0.00	0.00	2.52	2.30	UNK_AA692402	AA692402
116942_at	0.00	0.00	0.00	1.90	2.63	2.14	UNK_AI838939	AI838939
116963_at	0.00	0.00	0.00	2.77	3.27	0.00	UNK_AW125370	AW125370
116989_at	0.00	0.00	0.00	0.00	3.12	3.03	UNK_AI852587	AI852587
117030_at	0.00	0.00	0.00	0.00	5.28	4.57	UNK_AI838603	AI838603
117099_at	0.00	0.00	0.00	0.00	2.08	2.57	UNK_AI851714	AI851714

117145_at	0.00	0.00	0.00	0.00	4.05	3.74	UNK_AI850896	AI850896
117183_at	0.00	0.00	0.00	1.96	2.07	2.56	UNK_AI842864	AI842864
117207_at	0.00	0.00	0.00	0.00	6.29	4.16	UNK_AI854445	AI854445
117270_at	0.00	0.00	0.00	2.36	2.16	0.00	UNK_AI843596	AI843596
117277_at	0.00	0.00	0.00	1.82	5.08	7.60	UNK_AI850694	AI850694
129639_at	0.00	0.00	0.00	0.00	5.71	10.00	UNK_AW214378	AW214378
130183_at	0.00	0.00	0.00	2.33	1.64	3.07	UNK_AI643934	AI643934
130391_at	0.00	0.00	0.00	0.00	2.13	4.79	UNK_AI042932	AI042932
130507_at	0.00	0.00	0.00	0.00	2.01	3.69	UNK_AI846909	AI846909
131792_s_at	0.00	0.00	0.00	0.00	5.10	6.58	UNK_AI850822	AI850822
133116_at	0.00	0.00	0.00	0.00	3.46	5.36	UNK_AA754682	AA754682
134513_f_at	0.00	0.00	0.00	1.81	2.12	3.20	UNK_AI852600	AI852600
134631_at	0.00	2.91	0.00	3.80	0.00	0.00	UNK_AI154756	AI154756
134747_at	0.00	0.00	0.00	0.00	8.56	7.68	UNK_AI662497	AI662497
135131_at	0.00	0.00	0.00	0.00	5.42	5.34	UNK_AI508877	AI508877
135201_at	0.00	-3.44	-2.08	0.00	2.29	3.08	UNK_AA420078	AA420078
135263_at	0.00	0.00	0.00	0.00	2.50	10.32	UNK_AI850317	AI850317
135433_at	0.00	0.00	0.00	2.53	2.11	1.80	UNK_AI529496	AI529496
135743_at	0.00	0.00	0.00	0.00	6.47	10.98	UNK_AI849654	AI849654
136618_at	0.00	0.00	0.00	2.36	2.06	0.00	UNK_AW121395	AW121395
137046_s_at	0.00	1.74	0.00	0.00	4.40	7.29	UNK_AI854440	AI854440
138476_at	0.00	0.00	0.00	0.00	2.20	2.62	UNK_AI851865	AI851865
139147_at	0.00	0.00	0.00	0.00	3.32	7.41	UNK_AW121331	AW121331
139184_at	0.00	0.00	0.00	1.70	2.72	3.87	UNK_AI851432	AI851432
140220_r_at	0.00	0.00	0.00	3.07	2.67	0.00	UNK_AI846774	AI846774
140833_at	0.00	0.00	0.00	3.27	1.92	5.46	UNK_AI427839	AI427839
92233_at	0.00	0.00	0.00	1.91	1.90	2.14	UNK_AI098965	AI098965
92280_at	0.00	0.00	0.00	0.00	2.51	1.66	UNK_AA867778	AA867778
93018_at	0.00	0.00	0.00	0.00	3.93	0.00	UNK_AI790103	AI790103
93184_at	0.00	0.00	0.00	0.00	1.97	3.33	UNK_AI596362	AI596362
93187_at	0.00	1.31	0.00	1.91	1.60	2.47	UNK_AW048347	AW048347
93270_at	0.00	0.00	0.00	0.00	2.13	0.00	UNK_AI839918	AI839918
93283_at	0.00	0.00	0.00	0.00	2.65	0.00	UNK_AA869401	AA869401
93336_at	0.00	0.00	0.00	1.85	2.26	1.90	UNK_AW121539	AW121539
93471_at	0.00	1.62	0.00	0.00	1.78	2.03	UNK_AI594427	AI594427
93609_at	0.00	0.00	0.00	0.00	2.72	0.00	UNK_AA797709	AA797709
93719_at	0.00	0.00	0.00	0.00	1.88	5.54	UNK_AA050273	AA050273
93724_at	0.00	0.00	0.00	0.00	2.22	1.81	NTRKR2	AI596034
93805_at	0.00	0.00	0.00	0.00	2.64	1.86	UNK_AW121164	AW121164
93821_at	0.00	0.00	0.00	0.00	1.66	2.29	UNK_AW046101	AW046101
94019_at	0.00	0.00	0.00	1.98	1.94	2.15	UNK_AI852534	AI852534
94245_at	0.00	0.00	0.00	0.00	2.32	1.77	UNK_AW125865	AW125865
94253_at	0.00	0.00	0.00	2.26	1.54	0.00	UNK_AW061243	AW061243
94286_at	0.00	0.00	0.00	2.18	1.84	1.93	UNK_AW050340	AW050340
94367_at	0.00	1.90	1.65	0.00	2.11	0.00	UNK_AI850362	AI850362
94433_at	0.00	1.59	0.00	0.00	1.88	2.17	UNK_AW060684	AW060684
94514_s_at	0.00	0.00	0.00	0.00	2.14	1.91	UNK_AI853439	AI853439
94537_at	0.00	0.00	0.00	1.34	1.36	2.15	UNK_AI838859	AI838859
94771_at	0.00	2.20	0.00	0.00	0.00	0.00		0 AA178600
94842_at	0.00	0.00	0.00	0.00	2.22	0.00	UNK_AI853630	AI853630
94876_f_at	0.00	0.00	0.00	2.09	1.87	0.00	UNK_AI849207	AI849207
94963_at	0.00	0.00	0.00	2.09	1.75	0.00	UNK_AI462105	AI462105
95029_at	0.00	0.00	0.00	0.00	3.06	0.00	UNK_AW046747	AW046747
95094_g_at	0.00	0.00	0.00	0.00	2.20	1.98	UNK_AI035334	AI035334
95147_at	0.00	0.00	0.00	1.58	2.20	1.92	UNK_AI843795	AI843795
95393_at	0.00	0.00	0.00	0.00	2.53	0.00	UNK_AI503362	AI503362
95415_f_at	0.00	0.00	0.00	0.00	1.87	2.19	C1R	AI132585
95444_at	0.00	0.00	0.00	2.06	1.86	1.68	UNK_AW122274	AW122274
95604_at	0.00	0.00	0.00	0.00	3.22	0.00	UNK_AI843294	AI843294

95643_at	0.00	0.00	0.00	0.00	4.39	0.00	UNK_AW050287	AW050287
95675_at	0.00	0.00	0.00	0.00	1.94	2.96	UNK_AW121182	AW121182
95714_at	0.00	2.17	0.00	0.00	1.95	1.66	UNK_AI226264	AI226264
95939_i_at	0.00	3.03	0.00	0.00	1.49	0.00	UNK_AW047237	AW047237
96029_at	0.00	0.00	0.00	2.23	1.82	0.00	UNK_AI020542	AI020542
96155_at	0.00	0.00	0.00	0.00	3.63	0.00	UNK_AW049359	AW049359
96186_at	0.00	0.00	0.00	0.00	1.78	3.07	UNK_AI839286	AI839286
96269_at	0.00	0.00	1.65	2.04	0.00	0.00	UNK_AA716963	AA716963
96278_at	0.00	0.00	0.00	0.00	1.86	2.11	UNK_AI846553	AI846553
96329_at	0.00	0.00	0.00	2.29	1.95	0.00	UNK_AI837793	AI837793
96342_at	0.00	0.00	0.00	2.02	1.83	1.77	UNK_AI846320	AI846320
96516_at	0.00	0.00	0.00	0.00	2.55	0.00	UNK_AA960459	AA960459
96533_at	0.00	0.00	0.00	2.02	0.00	0.00	UNK_AI508931	AI508931
96609_at	0.00	0.00	0.00	2.00	1.79	1.94	UNK_AW122195	AW122195
96640_at	0.00	0.00	0.00	0.00	1.83	3.26	UNK_AI644158	AI644158
96698_at	0.00	0.00	0.00	0.00	2.18	0.00	UNK_AI835520	AI835520
96725_at	0.00	1.54	0.00	0.00	1.66	2.27	UNK_AI838398	AI838398
96739_at	0.00	0.00	0.00	0.00	3.08	0.00	UNK_AI852409	AI852409
96748_i_at	0.00	0.00	1.18	0.00	2.53	1.86	UNK_AA619554	AA619554
96762_at	0.00	0.00	0.00	0.00	1.87	2.00	UNK_AW046160	AW046160
96763_at	0.00	0.00	0.00	0.00	2.13	1.88	UNK_AI839995	AI839995
96773_at	0.00	0.00	0.00	2.49	1.75	0.00	UNK_AW125408	AW125408
96791_at	0.00	0.00	0.00	0.00	2.06	1.97	UNK_AW047875	AW047875
96827_at	0.00	0.00	0.00	0.00	4.81	0.00	UNK_AW061272	AW061272
96833_at	0.00	0.00	0.00	0.00	2.26	0.00	UNK_AW048468	AW048468
96854_at	0.00	0.00	0.00	1.95	2.13	1.77	COPA	AJ010391
97199_at	0.00	0.00	0.00	1.54	1.63	2.21	UNK_AI854767	AI854767
97217_at	0.00	0.00	0.00	1.78	1.76	2.16	UNK_AI842095	AI842095
97268_i_at	0.00	0.00	0.00	1.85	2.67	1.96	UNK_AI848699	AI848699
97359_at	0.00	0.00	0.00	0.00	2.10	1.85	UNK_AI851160	AI851160
97364_at	0.00	0.00	0.00	0.00	3.61	0.00	UNK_AW213865	AW213865
97423_at	0.00	0.00	0.00	0.00	2.28	0.00	UNK_AI839819	AI839819
97486_at	0.00	1.48	0.00	2.11	0.00	0.00	UNK_AA693246	AA693246
97704_at	0.00	0.00	0.00	0.00	3.14	0.00	0	AA414990
97713_at	0.00	0.00	0.00	0.00	2.23	0.00	UNK_AW214336	AW214336
97839_at	0.00	1.91	0.00	2.32	1.80	1.97	UNK_AI841960	AI841960
97865_g_at	0.00	0.00	0.00	0.00	1.98	3.57	UNK_AW258842	AW258842
97892_at	0.00	0.00	0.00	0.00	2.06	0.00	UNK_AI844732	AI844732
97903_at	0.00	0.00	0.00	0.00	3.15	0.00	UNK_AW050078	AW050078
97949_at	0.00	1.62	0.00	2.03	0.00	0.00	fibrinogen-like protein 2; Fgl2	M16238
97960_at	0.00	0.00	0.00	0.00	2.65	1.44	UNK_AW125800	AW125800
98051_at	0.00	0.00	0.00	0.00	1.60	2.00	GS15	AI852808
98431_at	0.00	0.00	0.00	0.00	3.32	0.00	UNK_AW049275	AW049275
98495_at	0.00	0.00	0.00	1.96	2.51	1.95	UNK_AI846906	AI846906
98528_at	0.00	0.00	0.00	0.00	2.15	1.48	UNK_AI854901	AI854901
98896_at	0.00	0.00	0.00	0.00	1.56	2.34	UNK_AW122980	AW122980
98948_at	0.00	0.00	0.00	0.00	2.77	0.00	UNK_AI785289	AI785289
98957_at	0.00	0.00	0.00	0.00	2.14	0.00	UNK_AI850297	AI850297
99062_at	0.00	0.00	0.00	0.00	3.03	1.64	UNK_AI891912	AI891912
99085_at	0.00	0.00	0.00	0.00	4.22	0.00	UNK_AI021421	AI021421
99949_at	0.00	0.00	0.00	0.00	2.36	0.00	UNK_AW060324	AW060324
99964_at	0.00	0.00	0.00	0.00	1.24	4.52	VDR	AW061016
100013_at	0.00	0.00	0.00	4.01	0.00	0.00	UNK_AW121732	AW121732
101291_at	0.00	0.00	0.00	0.00	3.69	0.00	UNK_Z83956	Z83956
101380_at	0.00	0.00	0.00	0.00	2.23	0.00	UNK_AW048282	AW048282
101591_at	0.00	0.00	0.00	0.00	2.20	1.69	UNK_AI852589	AI852589
102225_at	0.00	0.00	0.00	0.00	1.76	2.07	UNK_AA163268	AA163268
102360_at	0.00	0.00	0.00	0.00	2.84	1.89	UNK_AW214225	AW214225

102409_at	0.00	0.00	0.00	2.06	1.68	1.65	UNK_AW046963	AW046963
102421_at	0.00	0.00	0.00	0.00	2.16	0.00	UNK_AI847950	AI847950
102784_at	0.00	0.00	0.00	0.00	4.12	0.00	UNK_AI843949	AI843949
102870_at	0.00	0.00	0.00	0.00	2.37	1.98	UNK_AW125272	AW125272
102920_at	0.00	0.00	0.00	0.00	1.92	2.11	UNK_AW215585	AW215585
103079_at	0.00	0.00	0.00	0.00	1.91	2.50	UNK_AA982208	AA982208
103081_at	0.00	0.00	0.00	0.00	2.32	0.00	UNK_AA863928	AA863928
103203_f_at	0.00	0.00	0.00	0.00	2.37	0.00	UNK_AW259499	AW259499
103256_at	0.00	0.00	3.13	0.00	0.00	0.00	UNK_AI509811	AI509811
103308_at	0.00	0.00	0.00	0.00	4.17	0.00	UNK_AI450597	AI450597
103366_at	0.00	0.00	0.00	0.00	2.23	0.00	UNK_AI117236	AI117236
103562_f_at	0.00	0.00	0.00	0.00	2.69	0.00	0	M26005
103615_at	0.00	0.00	2.04	2.00	0.00	0.00	UNK_AA727023	AA727023
103711_at	0.00	0.00	1.74	0.00	1.84	2.04	UNK_AI115399	AI115399
103721_at	0.00	0.00	0.00	0.00	1.99	2.90	UNK_AA592182	AA592182
103734_at	0.00	0.00	0.00	0.00	2.20	1.58	UNK_AA985771	AA985771
103739_at	0.00	0.00	1.58	2.30	0.00	0.00	UNK_AW230977	AW230977
103744_at	0.00	0.00	0.00	0.00	2.22	1.40	UNK_AI852760	AI852760
103753_at	0.00	0.00	0.00	0.00	1.22	2.05	UNK_AI159572	AI159572
103890_at	0.00	0.00	0.00	0.00	3.96	0.00	UNK_AW050153	AW050153
103907_at	0.00	4.07	0.00	0.00	0.00	0.00	UNK_AW108492	AW108492
103916_at	0.00	0.00	0.00	0.00	2.19	1.81	UNK_AI850713	AI850713
104030_at	0.00	0.00	0.00	0.00	8.28	0.00	UNK_AI848841	AI848841
104042_at	0.00	0.00	0.00	0.00	3.78	0.00	UNK_AI842275	AI842275
104091_at	0.00	2.03	0.00	0.00	0.00	0.00	UNK_AW122563	AW122563
104110_at	0.00	0.00	0.00	0.00	2.15	1.59	UNK_AW060515	AW060515
104147_at	0.00	0.00	0.00	0.00	3.95	0.00	UNK_AW122052	AW122052
104179_at	0.00	1.51	1.70	1.78	2.12	1.67	UNK_AI788669	AI788669
104207_at	0.00	0.00	0.00	0.00	3.49	1.90	UNK_AI430272	AI430272
104222_f_at	0.00	0.00	0.00	0.00	2.00	0.00	0	C79210
104287_at	0.00	0.00	0.00	2.23	1.96	0.00	UNK_AI853807	AI853807
104303_i_at	0.00	0.00	0.00	0.00	2.18	0.00	UNK_AW124151	AW124151
104335_at	0.00	0.00	0.00	0.00	2.39	0.00	UNK_AW124084	AW124084
104339_at	0.00	0.00	0.00	0.00	2.57	0.00	UNK_AW060236	AW060236
104341_at	0.00	1.31	0.00	0.00	1.72	2.10	UNK_AW121406	AW121406
104351_at	0.00	0.00	0.00	0.00	9.17	0.00	UNK_AW120925	AW120925
104467_at	0.00	0.00	1.38	1.98	2.11	1.98	UNK_AA763004	AA763004
104525_at	0.00	0.00	0.00	0.00	1.67	2.50	UNK_AW124812	AW124812
104534_at	0.00	0.00	0.00	0.00	1.96	2.16	UNK_AA623874	AA623874
104561_at	0.00	0.00	0.00	0.00	4.63	0.00	UNK_AW120990	AW120990
104624_at	0.00	0.00	0.00	0.00	2.06	1.94	UNK_AI851539	AI851539
104634_at	0.00	0.00	0.00	2.03	1.40	1.80	UNK_AA874589	AA874589
104693_at	0.00	0.00	0.00	0.00	2.11	1.72	UNK_AA260145	AA260145
105160_at	0.00	0.00	0.00	0.00	2.09	1.80	UNK_AA739142	AA739142
105162_at	0.00	0.00	0.00	0.00	2.05	0.00	UNK_AW122704	AW122704
105165_at	0.00	0.00	0.00	1.77	4.74	0.00	UNK_AI562171	AI562171
105173_at	0.00	0.00	0.00	0.00	1.93	2.05	UNK_AI303628	AI303628
105184_at	0.00	0.00	0.00	0.00	2.19	1.69	UNK_AI639898	AI639898
105188_at	0.00	1.61	0.00	0.00	2.18	0.00	UNK_AI195930	AI195930
105209_at	0.00	0.00	0.00	0.00	1.48	2.54	UNK_AI159074	AI159074
105217_at	0.00	0.00	0.00	0.00	2.83	0.00	UNK_AI851943	AI851943
105326_at	0.00	0.00	0.00	0.00	1.57	2.06	UNK_AI836944	AI836944
105484_at	0.00	0.00	0.00	0.00	2.44	0.00	UNK_AW049561	AW049561
105506_at	0.00	0.00	0.00	2.62	0.00	0.00	UNK_AA217898	AA217898
105529_at	0.00	0.00	0.00	1.21	2.88	0.00	UNK_AW122385	AW122385
105688_f_at	0.00	0.00	0.00	2.07	1.60	0.00	UNK_AI842855	AI842855
105829_at	0.00	0.00	0.00	1.25	2.43	1.54	UNK_AW121238	AW121238
105842_at	0.00	0.00	0.00	0.00	3.02	0.00	UNK_AI841683	AI841683
105871_at	0.00	0.00	0.00	0.00	1.79	7.08	UNK_AI844617	AI844617

105953_at	0.00	0.00	0.00	0.00	1.91	2.74	UNK_AI839641	AI839641
105977_f_at	0.00	1.73	3.22	0.00	0.00	0.00	UNK_AA692591	AA692591
106019_f_at	0.00	0.00	0.00	0.00	2.36	0.00	UNK_AA823762	AA823762
106039_at	0.00	0.00	0.00	0.00	3.72	0.00	UNK_AA683764	AA683764
106113_at	0.00	0.00	0.00	0.00	2.04	0.00	UNK_AI850393	AI850393
106138_at	1.72	2.31	0.00	0.00	0.00	0.00	UNK_AA797808	AA797808
106175_at	0.00	0.00	0.00	0.00	1.73	4.48	UNK_AI851974	AI851974
106178_at	0.00	0.00	0.00	0.00	1.97	2.51	UNK_AW122268	AW122268
106208_at	0.00	0.00	0.00	0.00	2.84	0.00	UNK_AW123433	AW123433
106219_at	0.00	0.00	0.00	0.00	2.45	2.00	UNK_AW045938	AW045938
106263_at	0.00	0.00	0.00	0.00	2.84	1.79	UNK_AA591294	AA591294
106282_r_at	0.00	0.00	0.00	0.00	3.50	0.00	UNK_AI851600	AI851600
106538_at	0.00	0.00	0.00	2.68	1.80	0.00	UNK_AI647881	AI647881
106570_at	0.00	0.00	0.00	1.45	2.35	1.76	UNK_AI606458	AI606458
106574_at	0.00	0.00	0.00	1.71	2.03	0.00	UNK_AI837536	AI837536
106580_at	0.00	0.00	0.00	0.00	3.19	0.00	UNK_AI834858	AI834858
106592_at	0.00	0.00	0.00	2.22	0.00	0.00	UNK_AI115629	AI115629
106609_at	0.00	0.00	1.32	0.00	2.57	0.00	UNK_AA867207	AA867207
106650_at	0.00	0.00	0.00	2.17	0.00	0.00	UNK_AI841093	AI841093
106651_at	0.00	0.00	0.00	1.63	1.74	2.14	ADNP	AA790780
106673_at	0.00	0.00	0.00	0.00	2.65	0.00	UNK_AI839746	AI839746
106956_at	0.00	0.00	0.00	0.00	1.81	2.13	UNK_AW125566	AW125566
106998_at	0.00	0.00	0.00	0.00	5.51	0.00	UNK_AI845825	AI845825
107051_at	0.00	0.00	0.00	1.89	2.00	1.97	UNK_AI848855	AI848855
107067_at	0.00	0.00	0.00	0.00	3.06	0.00	UNK_AW047122	AW047122
107081_at	0.00	1.45	1.79	1.43	2.11	0.00	UNK_AA691890	AA691890
107105_at	0.00	0.00	0.00	1.82	1.64	2.54	UNK_AI159649	AI159649
107292_at	0.00	0.00	2.80	0.00	0.00	0.00	UNK_AW049900	AW049900
107348_at	0.00	0.00	0.00	0.00	2.06	0.00	UNK_AW050370	AW050370
107393_at	0.00	0.00	0.00	1.73	1.90	2.53	UNK_AI502997	AI502997
107412_at	0.00	0.00	0.00	0.00	4.17	0.00	UNK_AW048881	AW048881
107477_at	0.00	0.00	0.00	0.00	2.20	0.00	UNK_AW045655	AW045655
107478_at	0.00	2.14	0.00	0.00	0.00	0.00	UNK_AW048523	AW048523
107523_at	0.00	1.46	2.88	0.00	1.96	0.00	UNK_AW209229	AW209229
107558_at	0.00	0.00	0.00	0.00	3.76	0.00	UNK_AA833488	AA833488
107564_at	0.00	0.00	0.00	0.00	2.56	1.62	UNK_AW123129	AW123129
107571_at	0.00	0.00	0.00	2.21	1.65	0.00	UNK_AW122430	AW122430
107582_at	0.00	0.00	0.00	2.28	0.00	0.00	UNK_AW050026	AW050026
107617_at	0.00	0.00	0.00	0.00	2.66	0.00	UNK_AI851968	AI851968
107619_s_at	0.00	0.00	0.00	0.00	2.03	1.68	UNK_AW120573	AW120573
107677_at	0.00	0.00	0.00	0.00	2.58	0.00	UNK_AU023434	AU023434
107774_at	0.00	0.00	0.00	1.44	2.40	0.00	UNK_AI836428	AI836428
107810_at	0.00	0.00	0.00	0.00	2.27	0.00	UNK_AI847267	AI847267
107897_at	0.00	0.00	0.00	2.28	1.75	0.00	UNK_AI607556	AI607556
107938_at	0.00	0.00	0.00	1.58	2.31	0.00	UNK_AA881991	AA881991
107954_at	0.00	0.00	0.00	0.00	2.15	0.00	HOXA7	AW125404
107983_at	0.00	0.00	0.00	0.00	4.50	0.00	UNK_AI666712	AI666712
107988_at	0.00	0.00	0.00	0.00	2.07	0.00	UNK_AI849414	AI849414
108024_at	0.00	1.68	0.00	1.75	2.61	0.00	UNK_AA764623	AA764623
108028_at	0.00	0.00	0.00	0.00	2.41	0.00	UNK_AI606099	AI606099
108059_at	0.00	0.00	0.00	0.00	4.96	0.00	UNK_AI851960	AI851960
108087_at	0.00	0.00	0.00	0.00	1.59	2.07	UNK_AI837854	AI837854
108094_at	0.00	0.00	0.00	0.00	10.12	0.00	UNK_AI593656	AI593656
108302_at	0.00	0.00	0.00	0.00	2.11	0.00	PKCM	AW121285
108371_at	0.00	0.00	0.00	0.00	1.96	2.45	UNK_AA710403	AA710403
108420_at	0.00	0.00	0.00	0.00	4.97	0.00	UNK_AI036798	AI036798
108497_at	0.00	0.00	0.00	1.90	1.86	3.24	UNK_AW124152	AW124152
108536_at	0.00	0.00	0.00	2.28	0.00	0.00	UNK_AI850994	AI850994
108562_at	0.00	0.00	0.00	1.34	2.14	1.56	UNK_AI195240	AI195240

108957_at	0.00	0.00	0.00	0.00	2.01	1.43	UNK_AA419670	AA419670
109007_at	0.00	0.00	0.00	0.00	2.08	0.00	UNK_AA738680	AA738680
109012_at	0.00	0.00	0.00	0.00	2.34	0.00	UNK_AA000177	AA000177
109089_at	0.00	0.00	0.00	0.00	1.77	2.77	UNK_AA798970	AA798970
109360_at	0.00	0.00	0.00	0.00	3.03	0.00	UNK_AA170489	AA170489
109363_at	0.00	0.00	0.00	0.05	1.43	4.09	UNK_AI847526	AI847526
109380_at	0.00	0.00	0.00	3.87	0.00	0.00	UNK_AA638457	AA638457
109391_at	0.00	0.00	0.00	2.10	1.86	1.92	UNK_AI852273	AI852273
109407_at	0.00	0.00	0.00	0.00	2.41	0.00	UNK_AW121433	AW121433
109416_at	0.00	0.00	0.00	0.00	3.05	0.00	UNK_AI835646	AI835646
109491_at	0.00	0.00	0.00	2.02	1.52	1.87	UNK_AA759948	AA759948
109509_at	0.00	0.00	0.00	1.95	3.55	0.00	UNK_AI593229	AI593229
109512_at	0.00	0.00	0.00	6.81	0.00	0.00	UNK_AA185047	AA185047
109521_at	0.00	0.00	0.00	0.00	4.10	0.00	UNK_AW123386	AW123386
109603_at	0.00	0.00	0.00	0.00	2.06	1.91	UNK_AW214377	AW214377
109607_at	0.00	0.00	0.00	1.79	1.91	2.49	UNK_AW108059	AW108059
109616_f_at	0.00	0.00	0.00	1.79	2.16	0.00	UNK_AA681095	AA681095
109623_at	0.00	0.00	0.00	0.00	3.31	0.00	UNK_AA105708	AA105708
109640_at	0.00	0.00	0.00	0.00	1.81	3.66	UNK_AW124435	AW124435
109658_at	0.00	0.00	0.00	0.00	5.20	0.00	UNK_AA869355	AA869355
109721_at	0.00	0.00	0.00	0.00	3.40	0.00	UNK_AI839609	AI839609
109745_at	0.00	0.00	0.00	2.12	1.79	1.92	UNK_AI837264	AI837264
109791_at	0.00	0.00	0.00	0.00	4.95	0.00	UNK_AI605156	AI605156
109910_at	0.00	0.00	0.00	0.00	1.78	2.57	UNK_AW123519	AW123519
109918_at	0.00	0.00	0.00	0.00	1.27	3.04	UNK_AI427170	AI427170
110009_at	0.00	0.00	0.00	0.00	4.01	0.00	UNK_AI551083	AI551083
110015_at	0.00	0.00	0.00	0.00	2.46	0.00	UNK_AI385637	AI385637
110128_at	0.00	0.00	0.00	0.00	1.66	2.28	UNK_AI664407	AI664407
110184_at	0.00	0.00	2.39	0.00	1.96	0.00	UNK_AW123961	AW123961
110204_at	0.00	0.00	0.00	0.00	1.79	2.89	UNK_AW123924	AW123924
110341_at	0.00	0.00	0.00	0.00	2.26	0.00	UNK_AI851727	AI851727
110344_at	0.00	0.00	0.00	0.00	5.37	0.00	UNK_AW123792	AW123792
110422_at	0.00	0.00	0.00	0.00	2.24	0.00	UNK_AA896206	AA896206
110449_f_at	0.00	0.00	0.00	1.33	1.85	2.18	UNK_AI154580	AI154580
110541_at	0.00	0.00	0.00	0.00	1.90	2.62	UNK_AI643915	AI643915
110650_at	0.00	0.00	0.00	0.00	1.72	2.11	UNK_AA959574	AA959574
110689_at	0.00	0.00	0.00	0.00	2.46	0.00	ADSL	AI391284
110693_at	0.00	0.00	0.00	0.00	2.41	0.00	UNK_AW121941	AW121941
110719_at	0.00	0.00	0.00	2.30	0.00	0.00	UNK_AI839189	AI839189
110824_at	0.00	0.00	0.00	0.00	2.62	0.00	UNK_AW121315	AW121315
110830_at	0.00	1.67	0.00	2.06	0.00	0.00	UNK_AI021707	AI021707
111203_at	0.00	0.00	0.00	0.00	2.25	0.00	UNK_AI614021	AI614021
111262_at	0.00	0.00	0.00	0.00	1.91	2.61	UNK_AW061180	AW061180
111294_at	0.00	1.68	0.00	0.00	1.89	3.19	UNK_AA175446	AA175446
111312_at	0.00	0.00	0.00	0.00	3.20	0.00	UNK_AA693306	AA693306
111319_at	0.00	0.00	0.00	2.37	0.00	0.00	UNK_AW124761	AW124761
111322_at	0.00	0.00	0.00	0.00	1.52	2.36	UNK_AI842842	AI842842
111343_i_at	0.00	0.00	0.00	2.05	1.92	0.00	UNK_AI853582	AI853582
111352_at	0.00	0.00	0.00	2.36	1.72	0.00	UNK_AW215724	AW215724
111379_at	0.00	0.00	0.00	2.26	1.74	0.00	UNK_AI846352	AI846352
111397_at	0.00	0.00	0.00	0.00	3.13	0.00	UNK_AI844734	AI844734
111417_at	0.00	0.00	0.00	0.00	2.29	0.00	UNK_AA980507	AA980507
111428_at	0.00	0.00	0.00	0.00	3.95	0.00	UNK_AW226863	AW226863
111430_r_at	0.00	0.00	0.00	0.00	3.43	0.00	UNK_AW011836	AW011836
111459_at	0.00	0.00	0.00	0.00	5.62	0.00	UNK_AI429433	AI429433
111475_at	0.00	0.00	0.00	1.97	2.16	0.00	UNK_AA880439	AA880439
111533_at	0.00	0.00	0.00	0.00	3.92	1.16	UNK_AI843308	AI843308
111535_at	0.00	0.00	0.00	0.00	2.17	0.00	UNK_AI226156	AI226156
111543_at	0.00	0.00	0.00	0.00	2.28	0.00	UNK_AW122303	AW122303

111572_at	0.00	0.00	0.00	0.00	2.53	0.00	UNK_AA096501	AA096501
111578_at	0.00	0.00	0.00	1.97	2.98	0.00	UNK_AA110885	AA110885
111647_at	0.00	3.03	0.00	0.00	0.00	0.00	UNK_AI156274	AI156274
111685_at	0.00	0.00	0.00	0.00	3.14	0.00	UNK_AW228742	AW228742
111741_at	0.00	0.00	0.00	2.39	0.00	0.00	UNK_AW123268	AW123268
111772_at	0.00	0.00	0.00	0.00	3.96	0.00	UNK_AI122096	AI122096
111793_at	0.00	0.00	0.00	0.00	1.64	2.34	UNK_AA940547	AA940547
111800_at	0.00	0.00	0.00	0.00	1.63	2.14	UNK_AI839784	AI839784
111829_at	0.00	0.00	0.00	2.17	0.00	0.00	UNK_AW122867	AW122867
111850_at	0.00	1.74	0.00	0.00	3.22	0.00	UNK_AI839747	AI839747
111931_at	0.00	0.00	0.00	0.00	1.81	2.75	UNK_AW125297	AW125297
111939_at	0.00	0.00	0.00	0.00	2.02	0.00	UNK_AI286751	AI286751
111952_at	0.00	0.00	0.00	6.16	0.00	0.00	UNK_AW046394	AW046394
112018_at	0.00	0.00	0.00	1.59	2.06	0.00	UNK_AW049226	AW049226
112031_g_at	0.00	0.00	0.00	0.00	2.04	0.00	UNK_AW048852	AW048852
112032_at	0.00	0.00	0.00	0.00	1.43	4.48	UNK_AI838644	AI838644
112082_at	0.00	0.00	0.00	0.00	5.39	0.00	UNK_AI591941	AI591941
112091_at	0.00	0.00	0.00	0.00	4.52	0.00	UNK_AI426016	AI426016
112167_f_at	0.00	0.00	0.00	0.00	2.50	0.00	UNK_W96857	W96857
112209_at	0.00	0.00	0.00	0.00	2.64	0.00	UNK_AW122818	AW122818
112269_at	0.00	0.00	0.00	0.00	1.77	2.67	UNK_AW123962	AW123962
112291_r_at	0.00	1.64	1.80	0.00	2.57	1.43	UNK_AA655542	AA655542
112333_at	0.00	0.00	0.00	2.17	0.00	0.00	UNK_AI835570	AI835570
112338_at	0.00	0.00	0.00	0.00	3.04	0.00	UNK_AI846227	AI846227
112402_at	0.00	0.00	0.00	0.00	2.30	0.00	UNK_AW045953	AW045953
112404_at	0.00	0.00	0.00	0.00	2.70	0.00	UNK_AI844302	AI844302
112488_at	0.00	0.00	0.00	0.00	1.88	3.93	UNK_AW120970	AW120970
112499_at	0.00	0.00	0.00	0.00	4.01	0.00	UNK_AI172791	AI172791
112652_at	0.00	0.00	0.00	0.00	3.04	0.00	UNK_AA636643	AA636643
112703_at	0.00	0.00	0.00	0.00	2.26	0.00	UNK_AI846613	AI846613
112729_at	0.00	0.00	0.00	0.00	1.50	2.17	UNK_AA644819	AA644819
112733_at	0.00	4.52	0.00	0.00	0.00	0.00	UNK_AW212343	AW212343
112795_at	0.00	0.00	0.00	1.99	1.74	2.51	UNK_AI854434	AI854434
112827_at	0.00	0.00	0.00	2.50	0.00	0.00	UNK_AI847696	AI847696
112847_at	0.00	0.00	0.00	0.00	5.12	0.00	UNK_AW123508	AW123508
112857_g_at	0.00	0.00	0.00	0.00	1.74	3.22	UNK_AI852143	AI852143
112981_at	0.00	0.00	0.00	0.00	3.36	0.00	UNK_AW060744	AW060744
112989_at	0.00	0.00	0.00	0.00	2.84	0.00	UNK_AA940527	AA940527
113018_at	0.00	0.00	0.00	0.00	2.51	0.00	UNK_AA855540	AA855540
113021_at	0.00	0.00	0.00	1.68	1.90	2.98	UNK_AI840910	AI840910
113027_at	0.00	0.00	0.00	0.00	2.41	1.83	UNK_AA816040	AA816040
113043_at	0.00	1.39	2.10	1.81	1.90	0.00	UNK_AI429002	AI429002
113119_at	0.00	0.00	0.00	2.06	0.00	0.00	UNK_AI835854	AI835854
113186_at	0.00	0.00	0.00	0.00	1.98	2.98	UNK_AI852046	AI852046
113226_at	0.00	0.00	0.00	0.00	1.46	2.36	UNK_AW230690	AW230690
113228_at	0.00	0.00	0.00	3.05	0.00	0.00	UNK_AW120751	AW120751
113239_at	0.00	0.00	0.00	0.00	2.39	0.00	UNK_AW213684	AW213684
113285_at	0.00	0.00	0.00	0.00	5.51	0.00	UNK_AI850452	AI850452
113288_at	0.00	0.00	1.97	0.00	1.78	3.18	UNK_AA967846	AA967846
113328_at	0.00	0.00	0.00	1.93	1.72	2.18	UNK_AW214631	AW214631
113333_at	0.00	0.00	1.64	1.58	1.86	2.27	UNK_AA793994	AA793994
113443_r_at	0.00	0.00	0.00	1.85	2.32	0.00	UNK_AI429737	AI429737
113541_at	0.00	0.00	0.00	2.43	0.00	0.00	UNK_AI843578	AI843578
113548_at	0.00	0.00	0.00	0.00	2.22	1.41	UNK_AI844170	AI844170
113550_at	0.00	0.00	0.00	0.00	2.03	0.00	UNK_AI846429	AI846429
113574_at	0.00	0.00	0.00	0.00	3.35	0.00	UNK_AW049388	AW049388
113620_at	0.00	0.00	0.00	0.00	4.93	0.00	UNK_AW047525	AW047525
113629_at	0.00	0.00	0.00	0.00	2.74	0.00	UNK_AW047341	AW047341
113656_at	0.00	0.00	0.00	0.00	2.02	0.00	UNK_AW050247	AW050247

113657_at	0.00	0.00	0.00	0.00	2.44	0.00	UNK_AW048440	AW048440
113695_at	0.00	0.00	0.00	0.00	4.37	0.00	UNK_AW120861	AW120861
113728_at	0.00	0.00	0.00	0.00	1.99	2.07	UNK_AA915716	AA915716
113777_at	0.00	0.00	1.73	1.61	1.91	3.04	UNK_AW048627	AW048627
113863_at	0.00	0.00	0.00	0.00	3.00	0.00	UNK_AA014260	AA014260
113896_at	0.00	0.00	0.00	1.74	2.37	0.00	UNK_AI425640	AI425640
114001_at	0.00	2.63	0.00	0.00	0.00	0.00	UNK_AW211307	AW211307
114102_at	0.00	1.37	0.00	1.47	1.81	2.47	UNK_AW061165	AW061165
114140_at	0.00	0.00	0.00	0.00	2.55	0.00	UNK_AW214473	AW214473
114168_at	0.00	0.00	0.00	0.00	2.43	0.00	UNK_AW121266	AW121266
114323_at	0.00	0.00	0.00	0.00	3.13	0.00	UNK_AA756403	AA756403
114379_at	0.00	0.42	2.02	1.46	0.00	0.00	UNK_AI050351	AI050351
114461_at	0.00	0.00	1.58	1.62	2.81	0.00	UNK_AI874945	AI874945
114525_at	0.00	1.28	0.00	0.00	2.05	1.73	UNK_AA290482	AA290482
114667_at	0.00	0.00	0.00	0.00	2.62	1.66	UNK_AA399878	AA399878
114695_at	0.00	0.00	2.00	0.00	0.00	0.00	UNK_AI842428	AI842428
114698_at	0.00	0.00	0.00	2.51	0.00	0.00	UNK_AW120476	AW120476
114709_at	0.00	0.00	0.00	0.00	2.24	0.00	UNK_AI847047	AI847047
114718_at	0.00	0.00	0.00	0.00	2.28	0.00	UNK_AI267112	AI267112
114747_at	0.00	0.00	0.00	2.24	1.87	0.00	UNK_AI851384	AI851384
114830_at	0.00	0.00	0.00	1.59	1.90	2.41	UNK_AI847957	AI847957
114880_at	0.00	0.00	2.18	1.92	1.39	1.80	UNK_AW123237	AW123237
114955_at	0.00	0.00	0.00	0.00	1.75	2.50	UNK_AI314760	AI314760
114996_at	0.00	0.00	0.00	0.00	2.00	0.00	UNK_AA967301	AA967301
115032_i_at	0.00	0.00	0.00	1.76	2.89	1.84	UNK_AI848847	AI848847
115064_at	0.00	0.00	0.00	0.00	2.36	0.00	UNK_AI573356	AI573356
115091_at	0.00	0.00	0.00	3.34	0.00	0.00	UNK_AA647787	AA647787
115093_at	0.00	0.00	0.00	0.00	1.90	3.27	UNK_AI606104	AI606104
115112_at	0.00	0.00	0.00	0.00	5.07	0.00	UNK_AW050362	AW050362
115140_at	0.00	0.00	0.00	0.00	2.84	0.00	UNK_AW124719	AW124719
115153_at	0.00	0.00	0.00	0.00	1.70	2.94	UNK_AI789647	AI789647
115195_at	0.00	0.00	0.00	1.66	11.32	0.00	UNK_AI838694	AI838694
115212_at	0.00	0.00	0.00	2.24	0.00	0.00	UNK_AA856478	AA856478
115266_at	0.00	0.00	0.00	0.00	3.97	0.00	UNK_AI152744	AI152744
115333_at	0.00	0.00	0.00	1.27	6.94	0.00	UNK_AI593245	AI593245
115338_at	0.00	0.00	2.06	0.00	0.00	0.00	UNK_AI158964	AI158964
115354_at	0.00	0.00	0.00	0.00	3.71	0.00	UNK_AA895031	AA895031
115371_at	0.00	0.00	0.00	0.00	1.99	7.39	UNK_AI465535	AI465535
115402_at	0.00	0.00	0.00	0.00	2.68	0.00	UNK_AW120513	AW120513
115416_at	0.00	0.00	0.00	0.00	3.28	0.00	UNK_AA645547	AA645547
115449_at	0.00	0.00	0.00	0.00	1.77	5.16	UNK_AW049627	AW049627
115481_at	0.00	0.00	0.00	0.00	2.75	0.00	UNK_AI256692	AI256692
115506_at	0.00	0.00	0.00	0.00	1.60	2.05	UNK_AW048699	AW048699
115652_at	0.00	2.11	0.00	1.53	0.00	0.00	UNK_AI450439	AI450439
115885_at	0.00	0.00	0.00	0.00	2.93	0.00	UNK_AW211469	AW211469
115891_at	0.00	0.00	0.00	0.00	1.97	2.64	UNK_AI481691	AI481691
115898_at	0.00	0.00	0.00	0.00	3.98	0.00	UNK_AA739008	AA739008
115904_at	0.00	0.00	0.00	0.00	1.82	2.84	UNK_AI788994	AI788994
115916_at	0.00	0.00	0.00	0.00	1.32	2.42	UNK_AA691429	AA691429
115917_at	0.00	0.00	1.70	1.88	2.26	0.00	UNK_AA874421	AA874421
116044_at	0.00	0.00	0.00	1.94	2.10	0.00	UNK_AA824110	AA824110
116102_at	0.00	0.00	0.00	0.00	3.55	0.00	UNK_AW261562	AW261562
116139_at	0.00	0.00	0.00	0.00	3.24	0.00	UNK_AA838903	AA838903
116166_at	0.00	0.00	0.00	0.00	1.95	3.46	UNK_AI853928	AI853928
116286_at	0.00	0.00	0.00	2.20	1.92	0.00	UNK_AI553581	AI553581
116320_at	0.00	0.00	0.00	0.00	1.60	3.82	UNK_AW124054	AW124054
116345_at	0.00	0.00	1.80	1.61	2.25	0.00	UNK_AI854429	AI854429
116379_at	0.00	0.00	0.00	0.00	2.14	0.00	UNK_AA178683	AA178683
116386_at	0.00	0.00	0.00	0.00	3.10	0.00	UNK_AA981888	AA981888

116426_at	0.00	0.00	0.00	0.00	2.50	0.00	UNK_AW212535	AW212535
116431_at	0.00	0.00	0.00	0.00	2.17	0.00	UNK_AI316839	AI316839
116451_at	0.00	0.00	0.00	0.00	4.73	1.71	UNK_AA615200	AA615200
116562_at	0.00	2.64	0.00	0.00	0.00	0.00	UNK_AI451360	AI451360
116576_at	0.00	0.00	0.00	0.00	1.76	2.03	UNK_AI451563	AI451563
116582_at	0.00	0.00	0.00	0.00	2.90	0.00	UNK_AI987726	AI987726
116671_at	0.00	0.00	0.00	0.00	1.75	2.22	UNK_AW123023	AW123023
116831_at	0.00	0.00	0.00	0.00	2.29	0.00	UNK_AI747220	AI747220
116858_at	0.00	0.00	1.49	1.78	1.76	7.51	MAFB	AI849704
116955_at	0.00	0.00	0.00	0.00	2.46	0.00	UNK_AI847605	AI847605
116986_at	0.00	0.00	0.00	0.00	2.28	0.00	UNK_AW120935	AW120935
117186_at	0.00	1.72	1.60	2.17	1.62	0.00	UNK_AI847496	AI847496
117196_at	0.00	0.00	0.00	0.00	1.80	4.64	UNK_AI840220	AI840220
117218_at	0.00	0.00	0.00	0.00	3.04	0.00	UNK_AI848424	AI848424
117235_at	0.00	1.18	0.00	1.34	2.48	0.00	UNK_AI843866	AI843866
117260_at	0.00	0.00	0.00	0.00	4.03	0.00	UNK_AI841583	AI841583
117276_at	0.00	0.00	0.00	0.00	2.92	0.00	UNK_AI849085	AI849085
117310_at	0.00	0.00	0.00	0.00	3.99	0.00	UNK_AI835269	AI835269
129180_f_at	0.00	0.00	0.00	0.00	1.87	3.06	UNK_AW214234	AW214234
129925_at	0.00	0.00	0.00	0.00	1.88	3.42	UNK_AW212719	AW212719
129983_at	0.00	1.93	1.73	3.10	1.52	1.45	UNK_AA795716	AA795716
130549_f_at	0.00	6.37	0.00	0.00	0.00	0.00	UNK_AU018276	AU018276
130719_at	0.00	0.00	0.00	1.99	1.42	4.14	UNK_AW045814	AW045814
130804_at	0.00	0.00	0.00	1.73	2.86	0.00	UNK_AU024135	AU024135
132172_at	0.00	0.00	2.03	1.88	0.00	0.00	UNK_AI195127	AI195127
132364_i_at	0.00	0.00	0.00	0.00	2.40	0.00	UNK_AI594430	AI594430
132365_r_at	0.00	0.00	0.00	0.00	1.89	2.06	UNK_AI594430	AI594430
133139_at	0.00	0.00	0.00	3.87	1.76	0.00	UNK_AW122295	AW122295
133799_at	0.00	0.00	0.00	0.00	4.06	0.00	UNK_AI131700	AI131700
133901_f_at	0.00	0.00	0.00	1.64	0.46	2.10	UNK_AI481837	AI481837
134388_at	0.00	1.21	0.00	0.00	1.88	2.31	UNK_AI536536	AI536536
134515_at	0.00	0.00	0.00	0.00	1.93	2.29	UNK_AI874652	AI874652
134531_at	0.00	0.00	0.00	0.00	4.11	1.62	UNK_AW121822	AW121822
134597_at	0.00	0.00	0.00	0.00	4.14	0.00	UNK_AI643832	AI643832
134660_at	0.00	0.00	0.00	2.17	1.73	0.00	UNK_AA793588	AA793588
134662_f_at	0.00	0.00	0.00	2.20	1.47	1.48	UNK_AI585590	AI585590
135172_at	0.00	0.00	0.00	0.00	1.32	2.79	UNK_AI480578	AI480578
135314_at	0.00	0.00	1.79	1.78	2.48	2.00	UNK_AI842058	AI842058
135355_at	0.00	0.00	0.00	0.00	1.91	3.47	UNK_AW228646	AW228646
135552_f_at	0.00	2.62	0.00	0.00	0.00	0.00	UNK_AI646499	AI646499
135655_at	0.00	0.00	0.00	2.23	0.00	0.00	UNK_AI447921	AI447921
135812_at	0.00	0.00	0.00	0.00	2.23	0.00	UNK_AI848262	AI848262
135888_at	0.00	0.00	0.00	1.83	1.89	2.00	UNK_AI153331	AI153331
136132_at	0.00	1.92	2.10	1.78	0.00	0.00	UNK_AI853191	AI853191
136191_at	0.00	2.22	0.00	0.00	0.00	0.00	UNK_AI852455	AI852455
136558_at	0.00	0.00	0.00	0.00	1.01	2.20	UNK_AI465462	AI465462
137699_at	0.00	2.23	0.00	0.00	1.35	0.00	UNK_AW045500	AW045500
138079_at	0.00	0.00	0.00	0.00	1.62	2.50	UNK_AI849673	AI849673
138945_at	0.00	2.27	0.11	0.00	0.00	0.00	UNK_AI843433	AI843433
138960_f_at	0.00	0.00	0.00	0.00	1.25	2.04	UNK_AI841128	AI841128
140441_at	0.00	2.51	0.00	0.00	0.00	0.00	UNK_AW105899	AW105899
140654_at	0.00	0.00	0.00	0.00	1.49	2.03	UNK_AA967374	AA967374
140760_at	0.00	0.00	0.00	0.00	2.05	0.00	UNK_AI648116	AI648116
140893_at	0.00	0.00	0.00	1.17	2.24	0.00	UNK_AW123714	AW123714
140999_at	0.00	1.68	1.97	2.74	1.61	1.53	UNK_AA561076	AA561076
141179_at	0.00	2.26	0.00	0.00	0.00	0.00	UNK_AI645500	AI645500

97543_at	0.00	0.00	0.00	2.96	1.83	2.01	expressed, developmentally down-regulated gene 5; Nedd5	D49382
96337_at	0.00	0.00	0.00	0.00	6.05	6.35	PNUTL1	AF033350
98609_at	0.00	0.00	0.00	3.74	5.09	4.97	MSF	AJ250723
98149_s_at	0.00	2.78	2.86	6.13	9.13	4.99	UNK_AW046496	AW046496
110272_at	0.00	2.06	5.37	4.90	3.35	3.49	UNK_AA636558	AA636558
92459_at	0.00	4.73	9.59	15.62	24.77	14.53	UNK_AB023418	AB023418
97198_at	0.00	0.00	0.00	3.04	2.54	4.37	cassette, sub-family A (ABC1), member 1; Abca1	X75926
103035_at	0.00	1.73	2.92	4.20	2.83	4.90	TAP1	U60020
98402_at	0.00	0.00	0.00	2.12	2.32	2.07	ACLP7	AI843799
92688_at	0.00	2.01	2.65	2.91	2.26	2.58	acid phosphatase 2, lysosomal; Acp2	X57199
97904_at	0.00	1.93	1.98	3.64	2.94	3.68	UNK_AW123953	AW123953
96573_at	0.00	1.69	0.00	2.54	1.91	2.14	actin, gamma, cytoplasmic,actin-like; Actg,Actl	M21495
96343_at	0.00	1.72	1.82	3.41	3.64	3.03	UNK_AI836968	AI836968
93100_at	0.00	0.00	0.00	3.39	4.40	2.27	vascular smooth muscle; Actvs	X13297
93460_at	0.00	0.00	0.00	0.00	2.49	1.93	activin A receptor, type 1; Acvr1	L15436
100751_at	0.00	0.00	0.00	0.00	2.25	2.76	metalloprotease domain (ADAM) 10; Adam10	AF011379
92414_at	0.00	1.50	0.00	5.97	9.93	8.83	a disintegrin and metalloproteinase domain 12 (meltrin alpha); Adam12	D50411
103554_at	0.00	0.00	2.63	3.50	5.47	3.45	a disintegrin and metalloproteinase domain 19 (meltrin beta); Adam19	AA726223
103024_at	6.28	10.02	5.98	4.43	4.10	2.38	ADAM8	X13335
103392_at	0.00	0.00	2.42	3.39	3.92	3.18	adenylate cyclase 7; Adcy7	U12919
94535_at	0.00	0.00	0.00	0.00	2.19	0.00	ADD1	AW121844
100903_at	0.00	0.00	0.00	2.36	1.77	1.90	ADPRT2	AJ007780
99038_at	0.00	0.00	0.00	3.40	4.12	3.85	adenylosuccinate synthetase 2, non muscle; Adss2	L24554
99039_g_at	0.00	1.47	0.00	2.78	2.26	2.44	adenylosuccinate synthetase 2, non muscle; Adss2	L24554
100412_g_at	0.00	0.00	0.00	2.85	2.62	0.00	AEBP1	AF053943
136586_at	0.00	3.12	3.56	5.26	6.60	6.27	UNK_AA960336	AA960336
96357_at	0.00	1.61	1.85	2.83	3.78	4.62	AF007010	AW212775
104205_at	0.00	0.00	0.00	3.25	19.16	4.89	aggrecan, structural proteoglycan of cartilage; Agc	L07049
92210_at	0.00	0.00	0.00	0.00	2.69	7.02	Agpt2	AF004326
96025_g_at	0.00	0.00	2.18	2.51	0.00	0.00	adenosylhomocysteine hydrolase; Ahcy	L32836
103551_at	0.00	0.00	0.00	0.00	2.39	4.11	UNK_AW124208	AW124208
116577_at	0.00	0.00	0.00	0.00	2.86	3.71	UNK_AI450355	AI450355
107536_at	0.00	0.00	2.87	4.47	3.94	4.08	UNK_AI851964	AI851964

104415_at	0.00	0.00	0.00	0.00	2.85	0.00	UNK_AA833293	AA833293
103911_at	0.00	0.00	0.00	0.00	2.57	2.19	UNK_AI851573	AI851573
102330_at	2.21	4.90	6.74	9.69	5.41	3.36	AIF1	D86382
103443_at	0.00	2.98	0.00	0.00	2.23	0.00	UNK_AA711704	AA711704
95148_at	0.00	0.00	1.83	3.07	3.90	5.63	AK2	AB020202
92796_at	0.00	0.00	4.88	10.36	57.57	19.90	phosphatase 2, liver; Akp2	J02980
96888_at	0.00	0.00	0.00	2.21	2.04	2.03	UNK_AI839814	AI839814
100970_at	0.00	0.00	0.00	2.56	2.72	2.86	thymoma viral proto-oncogene; Akt	X65687
98372_at	0.00	2.97	0.00	5.29	2.86	0.00	UNK_AW050387	AW050387
96243_f_at	0.00	1.81	0.00	0.00	2.32	3.58	UNK_AW120804	AW120804
102048_at	4.83	7.77	16.74	18.48	10.36	4.40	ALRP	AF041847
94392_f_at	0.00	2.01	1.70	2.55	2.32	0.00	angiogenin; Ang	U22516
102054_at	0.00	2.71	0.00	2.96	2.56	2.75	ANKHZN	AB011370
93038_f_at	0.00	2.05	2.40	3.64	3.20	3.58	LPC1	M69260
100569_at	2.07	2.76	2.79	4.54	4.52	4.67	annexin A2; Anxa2	M14044
101393_at	2.43	0.00	0.00	2.45	2.13	0.00	ANXA3	AJ001633
100584_at	0.00	0.00	1.67	2.84	2.85	4.02	annexin A4; Anxa4	U72941
93083_at	0.00	0.00	0.00	2.67	2.69	2.86	ANXA5	D63423
93587_at	0.00	0.00	0.00	3.45	0.00	0.00	annexin A7; Anxa7	L13129
97529_at	0.00	2.06	0.00	5.97	8.79	7.30	annexin A8; Anxa8	AJ002390
102327_at	0.00	0.00	2.07	2.55	3.01	3.11	AOC3	AF078705
103242_at	0.00	0.00	0.00	1.94	2.49	2.90	UNK_AW123834	AW123834
103878_at	0.00	0.00	0.00	2.13	2.21	2.07	AP3B1	AF103809
103796_at	0.00	0.00	0.00	3.99	3.27	3.46	APAF1	AF064071
102710_at	2.15	2.86	3.37	3.90	3.45	5.22	precursor protein-binding, family B, member 1 interacting protein; Apbb1ip-pending	AF020313
101035_at	0.00	0.00	2.01	0.00	1.84	2.15	apoptosis inhibitor 5; Api5	U35846
98398_s_at	0.00	2.97	3.11	3.55	2.15	2.64	APOBEC1	U22262
95356_at	0.00	1.46	1.78	2.38	2.50	3.08	Apoe	D00466
93700_at	0.00	0.00	0.00	0.00	2.47	2.59	SIAT9	AI838022
96587_at	0.00	0.00	0.00	0.00	3.15	2.61	ADP-ribosylation factor 3; Arf3	D87900
92968_at	0.00	0.00	0.00	0.00	2.14	0.00	ADP-ribosylation factor 5; Arf5	D87902
93097_at	0.00	6.15	1.74	1.71	0.00	0.00	Arg1	U51805
101030_at	0.00	0.00	0.00	1.85	2.12	3.24	homolog B (RhoB); Arhb	X99963
96056_at	0.00	0.00	0.00	3.00	3.64	4.22	homolog 9 (RhoC); Arhc	X80638
95547_at	0.00	0.00	0.00	0.00	5.84	3.99	homolog D (RhoD); Arhd	D89821
98001_at	0.00	0.00	2.06	1.83	2.85	2.92	nucleotide exchange factor (GEF) 1; Arhgef1	U58203
101439_at	0.00	0.00	0.00	0.00	2.72	2.07	UNK_AW122716	AW122716
115479_at	0.00	0.00	2.38	5.55	5.94	3.35	ARP2-PENDING	AA792177
95434_at	0.00	2.17	2.13	2.92	2.24	2.57	UNK_AI851740	AI851740
100931_at	0.00	0.00	0.00	0.00	4.46	4.79	arylsulfatase A; As2	X73230
94282_at	0.00	1.86	0.00	3.66	3.84	3.64	UNK_AW124297	AW124297
95133_at	0.00	0.00	0.00	0.00	5.31	0.00	asparagine synthetase; Asns	U38940

101984_at	0.00	0.00	0.00	1.79	2.04	2.76	ATX1 (antioxidant protein 1) homolog 1 (yeast); Atox1	AF004591
99579_at	0.00	1.58	0.00	2.44	2.72	3.30	beta 3 polypeptide; Atp1b3	U59761
98126_s_at	0.00	0.00	0.00	0.00	2.12	0.00	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1; Atp2a1	X67140
95746_at	0.00	1.51	0.00	2.69	2.20	7.69	ATP6A2	AW123765
95745_g_at	0.00	1.35	0.00	1.80	1.68	6.74	transporting, lysosomal (vacuolar proton pump), alpha 70 kDa, isoform 2;	U13837
94301_at	0.00	2.37	2.07	3.22	5.34	8.96	ATP6K	AI843269
102854_s_at	0.00	2.19	0.00	0.00	0.00	0.00	ATPase, Cu++ transporting, alpha polypeptide; Atp7a	U03434
93984_at	0.00	1.88	2.24	3.26	3.23	3.67	Atpi	AF002718
98960_s_at	0.00	0.00	0.00	1.73	2.48	1.89	UNK_AF029792	AF029792
103002_at	0.00	0.00	0.00	1.95	2.15	1.84	B4GALT1	M27923
104005_at	0.00	0.00	0.00	0.00	5.00	2.43	B4GALT2	AB019541
111981_at	0.00	0.00	0.00	0.00	2.02	0.00	BACE2	AW122959
99670_at	0.00	0.00	0.00	0.00	3.45	2.81	Bcl-associated death promoter; Bad	L37296
93536_at	0.00	0.00	0.00	3.00	3.22	2.81	Bcl2-associated X protein; Bax	L22472
93252_at	0.00	0.00	0.00	0.00	2.57	0.00	B-cell receptor-associated protein 31; Bcap31	X81816
100026_at	0.00	0.00	0.00	5.43	16.18	0.00	BCAT1	U42443
94448_at	0.00	0.00	0.00	2.85	1.58	2.13	BCL10	AJ006289
102914_s_at	0.00	0.00	0.00	0.00	5.13	13.02	BCL2A1B	U23778
93869_s_at	0.00	0.00	0.00	2.68	3.36	9.35	BCL2A1D	U23781
101748_at	0.00	0.00	0.00	0.00	13.92	0.00	bradykinin receptor, beta; Bdkrb	U47281
101514_at	0.00	0.00	0.00	2.06	3.68	2.34	BET3-PENDING	AF041433
103647_at	0.00	0.00	3.61	2.66	5.42	16.86	beta-galactosidase complex; Bgl	M57734
96049_at	0.00	2.06	2.40	4.02	3.69	4.37	BGN	X53928
98433_at	0.00	2.16	0.00	0.00	1.45	2.01	domain death agonist; Bid	U75506
101521_at	0.00	4.32	4.05	5.67	5.14	3.35	API4	AB013819
95803_at	0.00	3.17	0.00	3.77	3.63	5.29	BIT	D85785
95804_g_at	0.00	5.17	0.00	0.00	8.80	10.32	BIT	D85785
93604_f_at	0.00	0.00	0.00	0.00	2.95	14.19	BL2	AF061260
93606_s_at	0.00	0.00	0.00	0.00	3.11	11.25	BL2	AB021966
95557_at	0.00	0.00	0.00	6.05	10.83	17.24	bone morphogenetic protein 1; Bmp1	L24755
92701_at	0.00	0.00	0.00	0.00	8.10	7.21	BMP1	AA518586
95012_at	0.00	0.00	0.00	0.00	1.54	4.40	UNK_AB012808	AB012808
98031_at	0.00	0.00	0.00	0.00	9.58	0.00	BOKL-PENDING	AF027707
94036_at	0.00	0.00	0.00	0.00	5.14	4.93	UNK_AI844806	AI844806
93324_at	0.00	0.00	0.00	3.98	3.49	3.40	butyrate response factor 1; Brf1	M58566
93104_at	0.00	2.95	2.80	4.02	4.75	5.01	BTG1	Z16410
96146_at	0.00	0.00	0.00	3.56	6.34	5.24	BTG3	D83745

104097_at	0.00	0.00	1.72	2.12	1.86	0.00	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae); Bub1	AF002823
109165_at	0.00	0.00	0.00	0.00	2.63	0.00	BUB1B	AW049504
93042_at	0.00	1.80	0.00	2.82	2.69	3.24	benzodiazepine receptor, peripheral; Bzrp	D21207
96718_at	0.00	0.00	0.00	0.00	1.79	2.12	UNK_AB012727	AB012727
98562_at	0.00	2.80	3.66	5.77	3.76	4.31	component 1, q subcomponent, alpha polypeptide;	X58861
96020_at	0.00	2.88	4.26	6.67	4.45	4.01	component 1, q subcomponent, beta polypeptide; C1qb	M22531
92223_at	0.00	1.85	2.43	4.07	2.93	2.85	component 1, q subcomponent, c polypeptide; C1qc	X66295
103707_at	0.00	2.61	3.37	4.05	3.10	2.93	C3AR1	U77461
103033_at	0.00	0.00	1.67	2.36	3.44	3.66	C4	X06454
101728_at	0.00	2.20	0.00	0.12	3.09	0.00	C5R1	S46665
98483_at	0.00	0.00	0.00	0.00	5.67	7.91	CACNB3	X94404
95423_at	0.00	2.15	2.96	5.11	3.94	3.37	CAI	Y00884
100155_at	3.86	2.01	2.63	4.29	1.65	0.00	Cak	L57509
101107_at	0.00	0.00	0.00	3.14	3.16	2.78	calumenin; Calu	U81829
104529_at	0.00	0.00	1.88	1.93	2.26	2.09	calcium modulating ligand; Caml	U21960
101040_at	0.00	1.47	1.28	2.06	1.74	2.07	calpain 2; Capn2	D38117
97942_g_at	-1.56	0.00	0.00	6.16	40.88	8.57	CAPN6	Y12582
97941_at	0.00	0.00	0.00	0.00	8.69	2.20	CAPN6	Y12582
97943_at	0.00	0.00	0.00	1.98	4.94	2.50	CAPN6	AI747133
93499_at	0.00	3.32	1.92	3.16	4.17	4.70	capping protein alpha 1; Cappa1	U16740
102248_f_at	0.00	1.87	0.00	2.83	3.31	2.91	CASK	Y17138
102064_at	0.00	1.72	0.00	2.05	1.38	2.48	CASP1	L28095
99049_at	0.00	0.00	0.00	0.00	2.36	3.08	caspase 2; Casp2	D28492
98436_s_at	0.00	0.00	2.32	3.29	4.63	3.72	apoptosis related cysteine protease; Casp3	U54803
94458_at	0.00	0.00	0.00	0.00	3.24	3.31	CASP6	Y13087
102328_at	1.67	0.00	3.82	0.00	5.01	4.40	CASP8	AJ007749
93364_at	0.00	1.84	0.00	2.26	2.32	2.91	CATNA1	X59990
98151_s_at	0.00	0.00	0.00	0.00	1.80	3.29	catenin src; Catns	Z17804
94817_at	0.00	2.19	2.44	4.38	4.24	4.34	CBP1	X60676
93697_at	0.00	0.00	0.00	0.00	1.72	3.53	CBX4	U63387
99186_at	0.00	8.48	3.62	3.94	5.08	3.50	CCNA2	X75483
94294_at	0.00	2.93	3.54	5.89	5.22	5.58	cyclin B2; Ccnb2	X66032
94232_at	0.00	2.12	1.47	1.84	2.61	2.72	CCND1	AI849928
99535_at	2.08	1.94	0.00	0.00	0.00	0.00	CCR4	AW047630
98153_at	0.00	0.00	0.00	2.04	1.83	0.00	chaperonin subunit 3 (gamma); Cct3	L20509
98446_s_at	0.00	1.83	1.75	2.36	1.70	0.00	EPHB4	U06834
98088_at	0.00	0.00	1.54	0.00	2.87	0.00	CD14 antigen; Cd14	X13333
103422_at	0.00	0.00	0.00	0.00	2.42	7.86	Cd1d1	M63695
101897_g_at	0.00	0.00	0.00	0.00	2.31	5.91	Cd1d2	M63697
103005_s_at	2.64	4.50	2.70	3.84	3.12	5.15	CD44	X66084
114697_at	2.65	4.08	3.95	6.25	8.24	22.18	CD44	AI594062
103089_at	0.00	4.30	5.56	6.22	5.21	4.03	CD48 antigen; Cd48	X53526
104606_at	2.11	3.68	3.52	4.72	4.14	7.46	CD52 antigen; Cd52	M55561

94939_at	2.23	3.23	3.49	4.50	3.47	5.59	CD53 antigen; Cd53	X97227
103016_s_at	0.00	2.52	3.48	6.07	4.53	15.71	CD68	X68273
101878_at	0.00	2.02	3.26	3.66	4.16	3.58	CD72 antigen; Cd72	J04170
99584_at	0.00	2.17	0.00	3.40	2.84	2.83	CD82 antigen; Cd82	D14883
103040_at	0.00	0.00	0.00	0.00	1.56	2.15	CD83	AI837100
95661_at	0.00	0.00	0.00	0.00	1.33	2.18	CD9	L08115
102934_s_at	0.00	1.60	0.00	2.80	2.37	0.00	CDC25C	L16926
100128_at	0.00	8.81	12.87	15.86	16.72	6.21	CDC2A	M38724
103821_at	0.00	1.77	1.70	1.97	2.01	0.00	CDC6	AJ223087
100006_at	0.00	0.00	0.00	0.00	6.64	5.01	CDH11	D21253
102852_at	0.00	0.00	0.00	0.00	7.68	9.75	cadherin 2; Cdh2	M31131
94412_at	0.00	0.00	0.00	0.00	2.88	3.60	CDK2	AJ223733
101017_at	0.00	0.00	0.00	0.00	3.17	2.52	CDK4	AA791962
100444_at	0.00	0.00	0.00	0.00	3.47	0.00	cyclin-dependent kinase 5; Cdk5	D29678
94881_at	0.00	0.00	0.00	0.00	3.11	0.00	CDKN1A	AW048937
98067_at	0.00	0.00	0.00	0.00	5.18	0.00	cyclin-dependent kinase inhibitor 1A (P21); Cdkn1a	U09507
95471_at	0.00	-2.68	-2.76	0.00	2.10	1.92	cyclin-dependent kinase inhibitor 1C (P57); Cdkn1c	U22399
101900_at	0.00	0.00	0.00	0.00	6.10	1.30	CDKN2B	AF059567
93094_at	0.00	0.00	0.00	0.00	3.46	3.26	degeneration-related 2; Cdr2	U88588
109137_at	0.00	0.00	0.00	0.00	3.39	3.25	CDYL	AI157065
100616_at	0.00	0.00	0.00	0.00	2.44	0.00	CENPA	AF012710
98770_at	0.00	0.00	0.00	0.00	2.24	0.00	CENPC	AF012708
107597_f_at	0.00	0.00	4.29	2.70	3.37	0.00	UNK_AA637016	AA637016
92788_f_at	0.00	0.00	0.00	2.36	2.67	2.72	CETN3	Y12474
93784_at	0.00	0.00	0.00	2.99	3.88	2.71	CFDP	AB010828
101853_f_at	0.00	0.00	0.00	0.00	3.42	11.91	component factor h; Cfh	M12660
92291_f_at	0.00	0.00	0.00	0.00	3.05	13.62	related protein; CFHRB	M29008
99119_at	0.00	2.89	3.39	4.99	6.15	6.26	cofilin 1, non-muscle; Cfl1	D00472
99120_f_at	0.00	0.00	0.00	2.06	2.24	1.88	cofilin 1, non-muscle; Cfl1	R75450
104509_at	0.00	1.89	0.00	0.00	2.34	0.00	CH25H-PENDING	AF059213
101459_at	0.00	0.00	0.00	0.00	1.60	2.02	helicase DNA binding protein 1; Chd1	L10410
103088_at	0.00	3.21	2.88	0.00	0.00	0.00	close homolog of L1; Chl1	X94310
100021_at	0.00	0.00	2.97	7.77	7.91	0.00	ACRA	M17640
96549_at	0.00	0.00	0.00	0.00	3.62	0.00	acetylcholine receptor delta; Acrd	L10076
102639_at	0.00	0.00	1.92	2.41	2.72	2.04	CHTS2	AB011451
92832_at	0.00	0.00	0.00	0.00	4.30	0.00	CISH1	U88325
92232_at	6.68	28.29	0.00	13.77	17.42	5.49	cytokine inducible SH2-containing protein 3; Cish3	U88328
93126_at	0.00	0.00	0.00	0.00	2.57	10.46	creatine kinase, brain; Ckb	X04591
97468_at	0.00	6.71	10.12	11.31	13.78	6.31	CKS1	AB025409
92762_at	2.53	6.19	4.80	3.95	2.46	3.99	CLECSF6	AJ133533
94256_at	0.00	2.07	2.20	3.05	4.36	3.47	CLIC4	AI849533
94254_at	0.00	0.00	1.62	2.70	2.24	3.40	CLIC4	AI845237

94255_g_at	0.00	1.55	1.90	2.51	1.93	3.71	CLIC4	AI845237
103346_at	0.00	0.00	0.00	0.00	2.31	2.73	CLK2	AF033564
100579_s_at	0.00	2.13	2.05	2.61	2.89	3.28	polypeptide (Lca); Clta	U91848
95286_at	0.00	1.77	0.00	2.24	0.00	0.00	CLU	D14077
102794_at	0.00	0.00	1.89	2.10	1.38	1.53	CMKAR4	Z80112
93397_at	2.34	4.18	3.03	4.05	2.45	3.21	chemokine (C-C) receptor 2; Cmkbr2	U56819
102718_at	2.24	3.99	3.37	0.00	2.71	0.00	CMKBR5	AF022990
102719_f_at	1.75	3.77	2.23	2.28	2.38	1.33	chemokine (C-C) receptor 5; Cmkbr5	X94151
94004_at	0.00	0.00	0.00	3.43	10.86	9.73	calponin 2; Cnn2	Z19543
100481_at	0.00	0.00	0.00	0.00	20.07	11.26	procollagen, type XI, alpha 1; Col11a1	D38162
103616_at	0.00	0.00	0.00	0.00	25.14	34.25	UNK_AF100956	AF100956
92314_at	0.00	0.00	0.00	0.00	10.67	0.00	XII, alpha 1; Col12a1	U25652
102261_f_at	0.00	0.00	0.00	0.00	2.65	4.65	COL13A1	U30292
102262_r_at	0.00	0.00	0.00	0.00	4.29	6.76	COL13A1	U30292
99476_at	0.00	0.00	0.00	1.84	2.80	2.91	COL14A1	AJ131395
99637_at	0.00	0.00	0.00	2.41	2.14	2.67	procollagen, type XV; Col15a1	AF011450
99638_at	0.00	0.00	0.00	3.24	5.40	5.62	procollagen, type XV; Col15a1	D17546
101881_g_at	0.00	0.00	0.00	4.81	10.82	10.32	COL18A1	L22545
102990_at	0.00	2.15	3.36	6.99	10.03	12.96	COL3A1	AA655199
98331_at	0.00	0.00	0.00	2.60	3.93	4.38	procollagen, type III, alpha 1; Col3a1	X52046
101093_at	0.00	0.00	0.00	2.28	2.02	2.23	COL4A1	M15832
101080_at	0.00	1.80	3.49	9.91	19.47	13.93	COL5A1	AB009993
101906_at	0.00	2.48	3.11	5.07	3.93	3.93	COL5A2	AA032310
92567_at	0.00	1.92	2.95	6.03	7.55	9.22	procollagen, type V, alpha 2; Col5a2	L02918
113235_at	0.00	0.00	0.00	2.96	1.95	3.12	COL5A3	AA734782
95493_at	0.00	0.00	0.00	3.72	3.84	3.50	procollagen, type VI, alpha 1; Col6a1	X66405
93517_at	0.00	0.00	1.99	4.43	6.38	5.80	COL6A2	Z18272
101110_at	0.00	0.00	2.32	5.51	6.14	5.80	COL6A3	AF064749
100308_at	0.00	2.74	2.14	6.75	37.35	14.46	procollagen, type VIII, alpha 1; Col8a1	X66976
104483_at	0.00	0.00	0.00	0.00	32.61	0.00	COL9A1	L12215
98027_at	0.00	0.00	0.00	0.00	4.61	0.00	procollagen, type IX, alpha 2; Col9a2	Z22923
102070_at	0.00	0.00	0.00	0.00	13.24	0.00	UNK_AW212495	AW212495
94305_at	0.00	0.00	0.00	2.82	0.00	0.00	COLA1	U03419
93340_f_at	0.00	0.00	0.00	4.50	3.30	2.24	COPB2	AF043120
93341_r_at	0.00	0.00	0.00	2.46	2.84	1.83	COPB2	AF043120
98930_at	0.00	0.00	0.00	0.00	2.06	0.00	UNK_AI844701	AI844701
110860_at	0.00	0.00	3.09	3.85	1.24	3.46	COPEB	AI846501
94427_at	0.00	0.00	0.00	2.68	4.76	3.81	COPG1	AI841737
96936_at	0.00	0.00	0.00	2.28	4.10	2.32	COPG1	AI020792
95149_at	0.00	0.00	0.00	2.58	1.86	2.06	UNK_AW121088	AW121088
104143_at	0.00	0.00	0.00	2.36	3.59	3.04	UNK_AI843212	AI843212
96648_at	0.00	13.50	4.26	0.00	5.51	6.88	CORO1A	AW122039
98928_at	0.00	1.68	0.00	3.37	5.06	5.56	CORO1B	AW122820
99631_f_at	0.00	1.54	0.00	2.84	2.08	3.07	COX6A1	U08440
92851_at	0.00	0.00	0.00	0.00	2.49	8.74	ceruloplasmin; Cp	U49430
95514_at	0.00	0.00	0.00	2.96	4.71	2.89	UNK_AI846302	AI846302

93320_at	0.00	1.78	2.64	3.70	2.65	3.94	carnitine palmitoyltransferase 1, liver; Cpt1a	AF017175
103492_at	0.00	0.00	0.00	0.00	10.90	5.75	UNK_AF077738	AF077738
98415_at	0.00	0.00	0.00	0.00	1.35	2.34	CREME9-PENDING	AF046060
98395_at	2.46	1.94	0.00	0.00	0.00	0.00	CRHR2	U21729
94061_at	0.00	0.00	0.00	2.64	1.93	2.29	intestinal protein; Crip	M13018
101879_s_at	0.00	0.00	0.00	0.00	1.75	2.34	CRRY	M23529
103817_at	0.00	2.19	2.37	5.07	8.57	7.80	UNK_AJ006469	AJ006469
92506_at	0.00	0.00	0.00	0.00	8.84	0.00	CRTL1	AF098460
101450_at	2.70	2.74	0.00	0.00	2.07	3.42	factor 1 (macrophage); Csf1	M21952
104354_at	0.00	2.65	3.08	4.25	2.85	6.88	factor 1 receptor; Csf1r	X06368
99330_at	0.00	2.37	2.21	3.33	2.11	4.32	factor 2 receptor, alpha, low-affinity (granulocyte-macrophage);	M85078
94284_at	0.00	0.00	0.39	3.31	2.27	2.13	UNK_AW122731	AW122731
103210_at	0.00	0.00	0.00	2.89	1.78	2.62	factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage);	M29855
104248_at	0.00	0.00	0.00	2.35	2.26	2.03	CSNK	AW227650
104249_g_at	0.00	0.00	0.00	1.76	2.15	1.71	CSNK	AW227650
100019_at	6.42	11.38	13.27	12.75	12.15	9.66	proteoglycan 2; Cspg2	D45889
92608_at	0.00	0.00	2.71	4.25	5.49	2.97	cysteine rich protein; Csrp	D88793
93550_at	0.00	2.70	4.70	12.96	26.37	8.78	cysteine-rich protein 2; Csrp2	D88792
100581_at	0.00	1.94	2.02	3.94	2.84	7.19	cystatin B; Cstb	U59807
92554_at	0.00	0.00	0.00	1.95	2.32	2.05	CTBP2	AF059735
100148_at	0.00	0.00	0.00	0.00	2.25	0.00	CCCTC-binding factor; Ctcf	U51037
96912_s_at	0.00	2.20	1.97	3.68	2.78	4.45	lymphocyte-associated protein 2 alpha; Ctla2a	X15591
103518_at	0.00	3.44	3.65	4.74	0.00	0.00	lymphocyte-associated protein 2 beta; Ctla2b	X15592
103341_at	0.00	1.78	2.25	2.07	1.92	0.00	triphosphate synthase; Ctps	U49350
101019_at	2.09	3.57	4.51	4.05	2.09	2.70	CTSC	U74683
101020_at	0.00	3.36	5.06	4.28	2.46	3.04	CTSC	AI842667
94834_at	0.00	1.76	2.32	4.76	5.57	5.93	cathepsin H; Ctsh	U06119
98543_at	0.00	1.80	2.38	3.24	2.52	4.10	CTSS	AJ223208
92633_at	0.00	1.52	2.44	2.98	2.97	6.50	D2WSU143E	AJ242663
94054_at	0.00	0.00	0.00	2.97	4.15	3.29	CTTN	AI841808
94055_at	0.00	0.00	2.52	0.00	5.91	4.16	cortactin; Cttn	U03184
97013_f_at	0.00	2.71	3.17	4.89	4.48	5.87	CYBA	AW046124
100059_at	0.00	2.19	2.49	3.52	3.30	4.51	alpha polypeptide; Cyba	M31775
100300_at	0.00	0.00	1.71	2.50	2.50	3.11	beta polypeptide; Cybb	U43384
99979_at	1.51	4.39	2.85	5.07	6.42	9.91	CYP1B1	X78445
94916_at	0.00	1.59	0.00	2.47	2.67	0.00	UNK_AW122260	AW122260

92777_at	0.00	2.49	3.85	4.95	3.04	1.84	cysteine rich protein 61; Cyr61	M32490
98619_at	0.00	0.00	0.00	0.00	3.27	0.00	UNK_AW121709	AW121709
106255_at	0.00	2.41	2.03	4.64	4.43	4.94	UNK_AI840993	AI840993
104358_at	0.00	0.00	0.00	1.86	5.05	0.00	UNK_AI853668	AI853668
107526_at	0.00	0.00	0.00	0.00	1.84	2.42	UNK_AA710084	AA710084
111683_at	0.00	0.00	0.00	2.21	2.79	4.85	D10UCLA1	AA153345
112407_at	0.00	0.00	0.00	0.00	2.20	3.03	D10UCLA1	AI021470
97824_at	0.00	1.87	2.19	2.60	2.50	1.64	UNK_AW121031	AW121031
94339_at	0.00	0.00	0.00	0.00	2.33	1.99	UNK_AI841330	AI841330
94242_at	0.00	0.00	0.00	2.16	1.70	1.68	UNK_AA881309	AA881309
93427_at	0.00	0.00	0.00	2.34	6.05	11.04	UNK_AW122310	AW122310
95480_at	0.00	0.00	0.00	0.00	2.18	0.00	D11WSU68E	AI847163
107600_at	0.00	0.00	0.00	1.79	2.58	0.00	UNK_AI838753	AI838753
111518_at	0.00	0.00	0.00	0.00	2.20	3.30	UNK_AA170647	AA170647
93775_at	0.00	0.00	0.00	1.81	1.83	2.23	UNK_AI841894	AI841894
98061_at	0.00	0.00	0.00	0.00	3.19	2.83	UNK_AI841192	AI841192
104558_at	0.00	0.00	0.00	0.00	4.22	3.13	D12WSU95E	AA867123
101372_at	0.00	0.00	0.00	2.81	2.01	0.00	UNK_AI852645	AI852645
98918_at	0.00	0.00	0.00	4.35	5.87	3.22	D13WSU115E	AI841920
94452_g_at	0.00	0.00	1.63	2.11	2.04	0.00	D13WSU123E	AI787627
94450_at	0.00	0.00	1.73	2.44	0.00	0.00	D13WSU123E	AI854202
94502_at	0.00	1.78	0.00	4.75	3.35	3.47	D13WSU50E	AW125724
104419_at	0.00	1.94	0.00	0.00	2.42	3.99	UNK_AI132380	AI132380
97325_at	0.00	0.00	0.00	2.68	2.67	2.97	UNK_AA881294	AA881294
94561_at	0.00	0.00	0.00	3.23	4.12	3.13	UNK_AI836140	AI836140
110414_at	0.00	0.00	0.00	2.05	5.26	3.81	UNK_AI594455	AI594455
111499_at	0.00	0.00	0.00	1.56	1.93	2.42	UNK_AW046236	AW046236
98013_at	0.00	1.88	2.52	0.00	3.28	3.54	UNK_AA666464	AA666464
114305_at	0.00	0.00	0.00	0.00	4.13	5.18	UNK_AA739238	AA739238
104633_at	0.00	4.17	3.44	3.82	3.73	2.71	D15WSU122E	AW123921
97822_at	0.00	0.00	0.00	0.00	3.38	2.85	UNK_AW122689	AW122689
97821_at	0.00	0.00	0.00	2.99	0.00	0.00	UNK_AI646056	AI646056
97823_g_at	0.00	0.00	0.00	0.00	1.81	2.08	UNK_AW122689	AW122689
95063_at	0.00	0.00	0.00	2.11	2.59	1.68	UNK_AI606257	AI606257
95137_at	0.00	3.19	3.65	7.69	11.28	4.71	UNK_AI852985	AI852985
97921_at	0.00	0.00	0.00	0.00	2.36	0.00	UNK_AI846279	AI846279
110388_at	0.00	0.00	0.00	0.00	2.12	0.00	UNK_AW213204	AW213204
115074_at	0.00	2.62	2.33	3.85	12.14	4.46	UNK_AI197311	AI197311
111433_at	0.00	0.00	0.00	2.83	5.30	0.00	UNK_AA795610	AA795610
109692_at	0.00	0.00	2.28	1.49	0.00	0.00	UNK_AI848006	AI848006
104333_at	0.00	6.18	7.27	7.18	9.71	6.35	DNA segment, Chr 17, human D6S56E 5; D17H6S56E-5	U69488
96318_at	0.00	0.00	0.00	3.10	4.21	3.13	D17WSU104E	AW045739
134595_at	0.00	0.00	0.00	2.88	2.15	2.49	UNK_AI006117	AI006117
100154_at	0.00	0.00	0.00	2.77	1.72	2.56	D17WSU91E	AI836367
104090_at	0.00	0.00	0.00	0.00	2.38	2.01	UNK_AA657164	AA657164
96346_at	0.00	-1.46	-2.12	0.00	2.45	5.93	D18UCLA3	AI854020
94967_at	0.00	0.00	0.00	0.00	1.66	3.20	UNK_AI851365	AI851365
96838_at	0.00	0.00	0.00	0.00	4.46	0.00	RCE1	AI851223
107005_at	0.00	0.00	0.00	1.90	3.19	0.00	UNK_AI853916	AI853916
113182_at	0.00	0.00	0.00	1.92	2.43	0.00	UNK_AI844871	AI844871
112787_f_at	0.00	0.00	0.00	2.64	2.54	2.82	UNK_AI838572	AI838572
112786_i_at	0.00	0.00	0.00	4.53	3.47	0.00	UNK_AI838572	AI838572
103310_at	0.00	0.00	0.00	0.00	2.12	1.91	0	AA220427
104740_at	0.00	0.00	0.00	0.00	2.41	2.78	UNK_AW125318	AW125318
95428_at	0.00	0.00	2.83	0.00	1.99	0.00	D1WSU40E	AA688761
104602_at	0.00	1.59	0.00	0.00	1.70	3.29	UNK_AW121972	AW121972

104640_f_at	0.00	0.00	0.00	2.44	2.40	2.19	UNK_AI464596	AI464596
104639_i_at	0.00	0.00	0.00	2.93	2.83	0.00	UNK_AI464596	AI464596
104225_at	0.00	0.00	0.00	0.00	2.10	2.21	UNK_AI645050	AI645050
100054_s_at	0.00	0.00	0.00	0.00	2.09	0.00	ENDOG	AW123127
107513_at	0.00	0.00	0.00	2.31	3.11	2.79	UNK_AW123087	AW123087
95708_at	0.00	2.11	3.22	5.70	7.02	8.87	UNK_AI843466	AI843466
98016_at	0.00	0.00	0.00	2.43	0.00	0.00	D3WSU161E	AA981268
95477_at	0.00	0.00	0.00	0.00	2.08	2.36	UNK_AW125185	AW125185
99621_s_at	0.00	2.08	2.54	2.56	2.88	2.85	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) (human)	AA690583
97295_at	0.00	2.47	4.02	4.10	3.48	2.80	UNK_AW122331	AW122331
104116_at	2.55	2.60	2.64	1.68	0.00	0.00	UNK_AW124049	AW124049
107574_at	0.00	0.00	0.00	2.45	2.15	3.00	UNK_AI836723	AI836723
98092_at	3.04	3.06	5.10	7.71	4.52	10.69	D5WSU111E	AA790307
104176_at	0.00	0.00	0.00	0.00	4.07	3.97	UNK_AI850941	AI850941
96675_at	0.00	0.00	0.00	1.94	2.68	2.48	UNK_AW124245	AW124245
104168_at	0.00	2.74	2.34	3.99	2.65	3.50	UNK_AA791742	AA791742
94237_at	0.00	2.35	3.47	5.76	4.82	3.95	D6WSU137E	AI846708
95541_at	0.00	2.27	0.00	4.67	5.62	5.12	D6WSU176E	AW125506
104300_at	0.00	1.95	2.90	6.09	4.75	5.14	IQGAP1	AI117936
95032_at	0.00	3.40	3.29	6.75	7.34	1.97	PRC1	AA856349
103871_at	0.00	0.00	0.00	3.06	3.70	1.44	UNK_AW123729	AW123729
110005_at	0.00	1.94	0.00	3.25	7.31	5.69	UNK_AA839741	AA839741
103862_r_at	0.00	0.00	0.00	2.45	2.02	2.13	D7WSU128E	AA388099
103861_s_at	0.00	0.00	0.00	2.07	2.29	0.00	D7WSU128E	AA388099
95709_at	0.00	0.00	0.00	3.89	6.25	6.07	D7WSU86E	AW012491
106634_at	0.00	0.00	0.00	2.10	0.00	0.00	UNK_AW123293	AW123293
96325_at	0.00	0.00	0.00	0.00	1.66	2.12	D8WSU108E	AW124874
95430_f_at	0.00	1.77	0.00	2.65	2.71	3.32	D9WSU18E	AI854154
98045_s_at	2.72	5.83	3.95	5.13	4.15	3.08	disabled homolog 2 (Drosophila); Dab2	U18869
98044_at	1.21	2.07	0.00	0.00	1.74	0.00	disabled homolog 2 (Drosophila); Dab2	U18869
96008_at	0.00	0.00	0.00	1.99	2.36	0.00	DAD1	U81052
117012_g_at	0.00	0.00	0.00	4.00	7.90	3.56	UNK_AW105743	AW105743
117011_at	0.00	0.00	0.00	0.00	3.01	0.00	UNK_AW105743	AW105743
103430_at	0.00	0.00	0.00	0.00	2.05	0.00	UNK_AW124952	AW124952
95529_at	0.00	1.86	2.09	5.10	2.54	3.94	drebrin-like; Dbnl	U58884
98071_f_at	0.00	2.00	3.67	3.69	3.07	3.72	deoxycytidine kinase; Dck	X77731
101104_at	0.00	0.00	0.00	1.46	1.46	2.07	critical region gene a; Dcra	AB001990
96636_at	0.00	1.43	1.65	2.07	1.84	1.97	UNK_AI852649	AI852649
95682_at	0.00	0.00	0.00	2.05	2.47	1.54	DDB1	AB026432
95683_g_at	0.00	0.00	0.00	1.88	2.50	1.80	DDB1	AB026432
100513_at	0.00	0.00	0.00	1.68	4.36	3.45	DDEF1	AF075461
101074_at	0.00	0.00	2.79	4.38	3.63	2.36	phosphooligosaccharide-protein glycotransferase; Ddost	D89063
103598_at	0.00	1.59	0.00	3.29	2.24	2.18	DDX9	U91922
131478_at	0.00	0.00	0.00	0.00	3.96	3.79	DECR2	AW120654
95688_at	0.00	1.75	1.72	2.39	2.05	2.52	spermatocyte homolog (Drosophila); Degs	Y08460
93188_at	0.00	0.00	0.00	4.20	11.48	5.36	DKK3	AJ243964

102207_at	0.00	0.00	0.00	0.00	3.35	3.26	UNK_AW123249	AW123249
101975_at	0.00	0.00	0.00	0.00	1.62	3.17	DLK1	Z12171
92332_at	0.00	0.00	2.88	0.00	2.22	0.00	distal-less homeobox 2; Dlx2	M80540
92930_at	0.00	0.00	0.00	0.00	8.22	7.47	distal-less homeobox 5; Dlx5	U67840
96703_at	0.00	1.79	3.01	7.33	9.33	5.98	UNK_AB029448	AB029448
103344_at	0.00	0.00	0.00	0.00	2.04	2.64	DnaJ-like protein 1; Dnajl1	L16953
99184_at	0.00	0.00	0.00	0.00	1.89	2.60	DNASE2	AW120896
96298_f_at	0.00	1.82	1.92	3.10	3.96	3.65	UNK_AF020185	AF020185
103030_at	0.00	0.00	0.00	4.57	7.87	4.91	dynamin; Dnm	L31397
103031_g_at	0.00	0.00	0.00	0.00	3.09	3.12	dynamin; Dnm	L31397
101445_at	0.00	2.65	0.00	0.00	0.00	0.00	DNMT	AF036008
113211_at	0.00	0.00	3.68	4.25	6.78	3.64	DNT-PENDING	AW049974
102896_at	0.00	0.00	2.04	3.64	4.81	3.43	tyrosine kinase 1; Dok1	U78818
102334_at	3.08	3.91	0.00	0.00	0.00	0.00	DOK2	AF059583
101503_at	3.58	3.12	4.04	8.95	7.81	5.99	dihydropyrimidinase-like 3; Dpysl3	X87817
102374_at	0.00	0.00	0.00	0.00	4.74	4.92	DSCR1L2	AI847661
97341_at	0.00	2.40	3.13	6.07	15.30	4.95	DXIMX39E	AW124082
96813_f_at	0.00	0.00	1.72	2.21	1.85	2.48	DXIMX46E	AI852973
112941_f_at	0.00	1.46	2.93	3.92	4.37	4.97	UNK_AA960514	AA960514
112940_i_at	0.00	0.00	0.00	2.74	5.32	7.05	UNK_AA960514	AA960514
115503_at	0.00	0.00	0.00	2.37	0.00	0.00	UNK_AI536452	AI536452
93306_at	0.00	1.46	0.00	2.07	1.87	1.74	polyposis coli binding protein Eb1; Eb1	U51196
96627_at	0.00	2.70	0.00	4.71	4.42	3.78	Ca2+ antagonist (emopamil) binding protein; Ebp	X97755
97411_at	0.00	2.04	3.41	2.85	4.03	1.78	ect2 oncogene; Ect2	L11316
92352_at	0.00	0.00	0.00	0.00	2.00	3.30	EDG3	AF108021
92867_at	0.00	0.00	0.00	0.00	4.47	3.82	EDR2	AF060076
113230_at	0.00	12.60	18.55	27.29	46.06	32.08	UNK_AW210333	AW210333
98407_at	0.00	0.00	0.00	0.00	4.30	3.00	ephrin B1; Efnb1	U07602
96195_at	0.00	0.00	0.00	0.00	2.74	5.31	embryonal Fyn-associated substrate; Efs	U57686
101842_g_at	0.00	0.00	0.00	0.00	2.82	0.00	EGFR	AW049716
115396_at	0.00	0.00	0.00	0.00	4.40	0.00	UNK_AW212285	AW212285
93058_at	0.00	2.41	2.49	4.00	4.26	3.39	UNK_AF026481	AF026481
103537_at	0.00	1.28	0.00	0.00	1.95	2.34	EIF2AK3	AF076681
99101_at	0.00	0.00	0.00	2.72	2.29	0.00	EIF3S7	AB012580
92816_r_at	0.00	1.75	1.97	0.00	2.95	2.45	EIF4A1	X03039
93783_at	0.00	0.00	0.00	0.00	2.98	0.00	0	M27347
99984_at	0.00	0.00	0.00	0.00	2.33	2.51	ELK3	L19953
101560_at	2.84	8.50	10.71	11.39	7.26	13.98	EMB	AW061330
97426_at	0.00	1.52	2.41	2.31	3.42	2.86	EMP1	X98471
93593_f_at	2.04	3.04	3.13	4.60	5.82	4.88	EMP3	U87948
103507_at	0.00	4.51	20.15	12.03	5.17	6.40	containing, mucin-like, hormone receptor-like sequence 1; Emr1	X93328
100134_at	0.00	0.00	0.00	4.01	4.92	4.32	endoglin; Eng	X77952
106642_at	0.00	0.00	1.68	0.00	3.70	1.79	UNK_AW260744	AW260744

104174_at	0.00	0.00	0.00	5.50	8.69	10.09	phosphodiesterase I/nucleotide pyrophosphatase 1; Pdnp1	J02700
115369_at	0.00	0.00	2.74	4.43	7.92	3.04	EPB4.1L3	AI835976
96623_at	0.00	2.54	2.75	4.70	5.02	3.50	EPCS21-PENDING	AI853172
103980_at	0.00	0.00	0.00	0.00	4.49	0.00	Epha2	U07634
95298_at	0.00	0.00	0.00	0.00	3.47	1.35	Epha3	M68513
93469_at	0.00	0.00	0.00	0.00	6.34	0.00	EPHB3	Z49086
104482_at	0.00	0.00	0.00	0.00	6.75	0.00	epimorphin; Epim	D10475
98992_at	0.00	0.00	0.00	2.10	3.71	0.00	EPPB9-PENDING	AB030483
104006_at	0.00	2.64	0.00	0.00	0.00	0.00	factor receptor pathway substrate 15; Eps15	L21768
93670_at	0.00	0.00	0.00	4.02	4.90	3.90	ERF	AW048233
94040_at	0.00	1.72	0.00	2.76	2.29	1.74	rudimentary *homolog* (Drosophila); Erh	D73368
98129_at	0.00	1.68	0.00	4.36	7.07	5.75	UNK_AI852553	AI852553
113283_at	0.00	0.00	2.92	3.42	2.28	4.63	ESTM25	AI036047
113563_at	0.00	0.00	0.00	0.00	2.14	2.15	ESTM3	AI845154
100348_at	0.00	0.00	3.31	0.00	3.48	2.28	ESTM4	AW214136
98025_at	1.99	3.06	3.68	5.90	5.31	4.61	integration site 2; Evi2	M34896
98026_g_at	0.00	2.64	3.50	4.48	4.34	4.88	integration site 2; Evi2	M34896
94810_at	0.00	1.61	0.00	2.32	2.75	2.25	Ewing sarcoma homolog; Ewsh	X79233
102811_at	0.00	1.49	2.88	2.92	4.07	10.13	exostoses (multiple) 1; Ext1	X96639
141160_f_at	0.00	0.00	0.00	10.92	7.94	16.18	EXT1	AA710704
99929_at	0.00	0.00	0.00	0.00	2.47	2.05	EXT2	U72141
99917_at	0.00	0.00	2.33	2.28	2.10	0.00	enhancer of zeste homolog 2 (Drosophila); Ezh2	U52951
95313_at	0.00	0.00	0.00	0.00	2.80	5.33	UNK_AW046032	AW046032
98967_at	0.00	6.61	7.73	7.50	4.13	2.08	protein 7, brain; Fabp7	U04827
98588_at	0.00	0.00	0.00	2.92	5.68	4.75	FAH	Z11774
92441_at	0.00	0.00	0.00	1.93	5.31	12.02	FAP	Y10007
96119_s_at	0.00	0.00	0.00	0.00	3.68	4.93	UNK_AA797604	AA797604
102114_f_at	0.00	0.00	0.00	0.00	3.74	7.50	UNK_AI326963	AI326963
94309_g_at	0.00	0.00	0.00	0.00	1.66	2.46	fibulin 1; Fbln1	X70853
101090_at	0.00	1.63	0.00	3.44	2.92	3.24	fibrillin 1; Fbn1	L29454
103623_at	0.00	0.00	0.00	-0.04	3.50	0.00	fibrillin 2; Fbn2	L39790
130689_at	0.00	1.99	0.00	4.20	3.52	0.00	FBXO17	AI957104
102879_s_at	2.15	2.81	3.04	3.28	2.15	0.00	Fc receptor, IgG, high affinity I; Fcgr1	M31314
101793_at	9.28	18.31	11.96	6.48	1.72	0.00	FCGR1	X70980
102337_s_at	0.00	6.07	3.61	4.74	4.61	2.61	FCGR2B	M31312
97327_at	0.00	2.17	3.19	3.45	1.91	0.00	specific endonuclease 1;	L26320
92188_s_at	0.00	0.00	0.00	1.71	2.16	2.22	feline sarcoma oncogene; Fes	X12616
93674_at	0.00	0.00	0.00	2.36	3.64	0.00	dysplasia homolog; Fgd1	U22325
115755_g_at	0.00	0.00	2.87	3.03	0.00	0.00	FGD2	AA958624
97509_f_at	0.00	0.00	0.00	0.00	2.00	2.61	FGFR1	U22324
93090_at	0.00	2.25	0.00	0.00	15.83	12.11	FGFR2	M23362

93091_s_at	0.00	0.00	0.00	0.00	12.79	8.09	factor receptor 2; Fgfr2	M63503
100884_at	0.00	8.62	5.24	11.29	12.67	10.44	factor regulated protein; Fgfrp	U04204
108539_at	1.30	2.97	3.41	3.92	1.57	0.00	FGFRP2-PENDING	AI853558
100986_at	0.00	0.00	0.00	1.61	2.26	2.55	FHL2	AF055889
99176_at	0.00	0.00	0.00	0.00	2.80	2.04	UNK_AI843393	AI843393
97421_at	0.00	3.18	3.75	4.37	5.50	2.59	factor inducible 16; Fin16	U42385
93294_at	6.49	4.31	6.60	6.52	9.13	4.84	secreted protein; Fisp12	M70642
103248_at	0.00	0.00	0.00	0.00	4.54	0.00	FKBP1B	AF060872
99546_at	0.00	2.31	0.00	3.07	2.84	2.41	protein 2 (13 kDa); Fkbp2	M77831
99082_at	0.00	2.02	2.88	8.30	16.01	13.94	protein 6 (65 kDa); Fkbp6	L07063
104746_at	0.00	0.00	0.00	4.08	8.21	6.92	FKBP7	AF040252
93731_at	0.00	0.00	0.00	2.75	3.90	3.42	FKBP9	AF090334
98441_at	0.00	2.19	2.46	3.50	3.23	2.83	retardation syndrome 1 homolog; Fmr1	L23971
104172_at	0.00	1.74	2.18	2.78	1.72	0.00	folate binding protein 2; Folbp2	M64817
92838_at	0.00	0.00	0.00	0.00	2.65	0.00	FSCN1	L33726
98817_at	0.00	2.64	0.00	0.00	4.80	0.00	follistatin; Fst	Z29532
105369_at	0.00	0.00	2.20	2.45	3.39	3.07	UNK_AW123943	AW123943
94833_at	0.00	1.28	0.00	3.60	2.58	3.49	follistatin-like; Fstl	M91380
103394_at	1.84	3.58	3.01	6.10	4.57	16.04	containing ion transport regulator 5; Fxyd5	U72680
100133_at	0.00	0.00	0.00	2.50	2.89	3.88	FYN	M27266
93681_at	0.00	0.00	0.00	5.25	7.24	0.00	UNK_AW123618	AW123618
97531_at	0.00	0.00	0.00	15.58	0.00	0.00	G0/G1 switch gene 2; G0s2	X95280
97516_at	0.00	2.18	2.47	4.38	4.79	5.05	alpha glucosidase 2, alpha neutral subunit; G2an	U92793
101294_g_at	0.00	3.52	2.38	0.00	1.94	3.20	G6PD2	Z84471
102292_at	2.03	2.13	1.47	0.00	0.00	0.00	DDIT1	U00937
101979_at	2.21	2.10	0.00	2.23	2.97	0.00	GADD45G	AF055638
109336_at	0.00	0.00	0.00	0.00	3.83	0.00	GADD45G	AI035425
103367_at	0.00	2.04	0.00	0.00	2.18	2.73	UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide-beta-1, 4-N-acetylgalactosaminyl transferase; Galgt1	U18975
115517_at	0.00	1.62	0.00	0.00	3.39	3.09	GALNS	AI845504
94338_g_at	0.00	0.00	0.00	0.00	2.27	0.00	growth arrest specific 2; Gas2	M21828
98530_at	0.00	0.00	0.00	0.00	3.47	2.41	GAS5	AI849615
98531_g_at	0.00	0.00	0.00	2.10	2.16	1.73	GAS5	AI849615
99067_at	0.00	1.65	1.75	2.27	2.93	2.61	growth arrest specific 6; Gas6	X59846
100488_at	0.00	0.00	0.00	2.15	2.08	2.54	acid beta glucosidase; Gba	M24119
103202_at	0.00	0.00	3.29	4.08	1.83	3.84	GBP3	AW047476
114351_at	0.00	0.00	0.00	1.71	2.75	4.42	GCL	AA727943

92655_at	0.00	0.00	0.00	2.20	1.93	0.00	glucosaminyl (N-acetyl) transferase 1, core 2; Gcnt1	U19265
109332_at	0.00	0.00	0.00	1.55	2.61	0.00	UNK_AW046226	AW046226
103590_at	0.00	0.00	0.00	2.29	5.83	3.68	UNK_AI507104	AI507104
93575_at	0.00	0.00	0.00	0.00	2.41	3.91	GGH	AF051102
102993_at	0.00	0.00	0.00	3.30	3.20	2.75	glycoprotein galactosyltransferase alpha 1, 3; Ggta1	M85153
100064_f_at	0.00	2.51	1.94	4.11	5.60	7.77	GJA1	M63801
100065_r_at	0.00	2.36	1.96	3.86	7.28	15.07	GJA1	M63801
104016_at	0.00	2.45	0.00	0.00	0.00	0.00	gap junction membrane channel protein beta 5; Gjb5	M91236
100395_at	0.00	0.00	0.00	0.00	2.10	0.00	GLI-Kruppel family member GLI2; Gli2	X99104
97820_at	0.00	0.00	2.46	3.78	9.89	2.84	GLK	AB027012
99141_at	0.00	0.00	0.00	1.91	1.71	4.95	activator protein; Gm2a	U09816
111347_at	0.00	0.00	0.00	2.18	2.61	3.02	UNK_AI842321	AI842321
112203_at	0.00	0.00	2.28	0.00	3.41	3.74	UNK_AI159117	AI159117
97227_at	0.00	0.00	0.00	0.00	2.05	0.00	guanine nucleotide binding protein, alpha 12; Gna12	M63659
97195_at	0.00	0.00	0.00	0.00	1.55	2.31	binding protein, alpha inhibiting 1; Gnai1	U38501
99597_at	0.00	3.19	1.89	3.28	2.96	3.96	GNAI2	AI841629
99596_f_at	0.00	1.55	0.00	2.57	2.74	2.78	binding protein, alpha inhibiting 2; Gnai2	M13963
99598_g_at	0.00	1.78	1.70	2.78	2.19	2.94	GNAI2	AI841629
98403_at	0.00	0.00	0.00	0.00	2.76	0.00	binding protein, related sequence 1; Gna-rs1	X65026
94854_g_at	0.00	0.00	1.55	2.04	2.09	2.16	guanine nucleotide binding protein, beta 1; Gnb1	U29055
97458_at	0.00	0.00	0.00	2.21	2.02	2.23	GNB1	AI845935
94853_at	0.00	0.00	0.00	2.38	1.75	2.56	guanine nucleotide binding protein, beta 1; Gnb1	U29055
96911_at	0.00	1.70	0.00	2.58	2.86	2.20	guanine nucleotide binding protein, beta 2; Gnb2	U34960
107026_at	0.00	0.00	1.56	1.38	2.66	2.01	UNK_AW123052	AW123052
93949_at	0.00	0.00	0.00	1.26	2.32	1.69	guanine nucleotide binding protein, beta 4; Gnb4	M63658
99175_at	0.00	1.95	0.00	3.06	3.53	3.40	GNG10	AI843396
100418_at	0.00	0.00	0.00	0.00	2.34	0.00	GNG2	AW123750
104469_at	0.00	3.50	3.20	3.84	3.87	3.68	Gp38	M73748
100325_at	2.62	2.49	3.65	4.12	4.79	5.72	glycoprotein 49 A,glycoprotein 49 B; Gp49a,Gp49b	M65027
92217_s_at	2.14	2.62	2.84	3.41	3.42	3.67	Gp49b	U05265
100435_at	0.00	0.00	0.00	0.00	6.50	2.76	GPCR26	U13370
96978_at	0.00	0.00	0.00	0.00	2.31	2.20	GPH-PENDING	AB025258
92611_at	0.00	1.62	2.76	2.64	3.18	2.91	P137	U18773

102040_at	0.00	0.00	0.00	0.00	6.38	0.00	GPRK6	Y15798
104257_g_at	1.81	3.32	4.39	2.84	3.70	4.44	UNK_AI120844	AI120844
93690_at	0.00	0.00	0.00	0.00	5.63	2.81	GRB10	AF022072
93691_s_at	0.00	0.00	0.00	1.82	5.28	2.39	receptor bound protein 10; Grb10	U18996
92263_at	0.00	0.00	0.00	3.94	7.69	6.29	leucine rich protein, B7 gene; Lrpb7	AC002397
94217_f_at	0.00	1.72	0.00	2.30	2.06	1.45	leucine rich protein, B7 gene; Lrpb7	AC002397
103993_at	0.00	0.00	0.00	0.00	4.50	3.02	leucine rich protein, B7 gene; Lrpb7	AC002397
130710_at	0.00	0.00	0.00	0.00	2.21	3.04	UNK_AA869432	AA869432
93066_at	0.00	2.00	3.08	4.01	3.19	5.73	GRN	D16195
95348_at	0.00	3.06	0.00	0.00	0.00	0.00	Gro1	J04596
108045_at	0.00	0.00	4.00	8.85	37.24	14.80	UNK_AA798520	AA798520
101060_at	0.00	1.98	2.32	4.79	4.52	3.76	reticulum protein; Erp	M73329
98052_at	0.00	0.00	0.00	2.10	3.20	2.28	GS15	AF003999
94369_at	0.00	0.00	0.00	0.00	2.95	3.81	GSNPAT-PENDING	AW123026
94811_s_at	0.00	0.00	0.00	3.37	1.72	0.00	factor IIH, polypeptide 1 (62kD subunit); Gtf2h1	AJ002366
93588_at	0.00	0.00	0.00	3.44	3.31	4.17	Gtl3	Z54179
98410_at	0.00	0.00	0.00	2.35	1.93	2.75	GTPI	AJ007972
98950_at	0.00	0.00	0.00	1.95	1.89	2.29	GTR2	AB017616
103038_at	0.00	0.00	0.00	1.95	2.54	2.11	guanylate cyclase activator 1a (retina); Guca1a	L36860
97538_at	0.00	2.21	3.31	4.47	4.17	7.37	GUS-S	M19279
102688_f_at	0.00	0.00	0.00	0.00	17.31	0.00	GZMD	X56990
102728_f_at	0.00	0.00	0.00	0.00	15.71	0.00	GZME	M36901
92866_at	0.00	2.07	0.00	2.67	2.11	4.52	H2-AA	X52643
100998_at	0.00	3.08	0.00	3.81	2.27	3.97	H2-AB1	M21932
94805_f_at	0.00	2.32	2.24	3.40	2.34	1.33	UNK_M33988	M33988
93019_at	0.00	0.00	1.29	2.00	3.96	1.92	HIST5-2AX	Z35401
101954_at	0.00	0.00	0.00	2.47	2.13	1.72	H2afz	U70494
97541_f_at	0.00	0.00	0.00	2.94	2.21	4.21	D region locus 1; H2-D	X00246
97540_f_at	0.00	0.00	0.00	2.17	1.64	2.90	D region locus 1; H2-D	M69069
101886_f_at	0.00	1.56	1.67	2.67	2.22	3.64	H2-L	X52490
98035_g_at	0.00	4.04	0.00	0.00	2.47	9.55	H2-DMB1	U35330
98034_at	0.00	1.58	0.00	0.00	2.12	0.00	H2-DMB1	U35330
94285_at	0.00	2.10	0.00	2.71	2.02	3.96	class II antigen E beta; H2-Eb1	X00958
97173_f_at	0.00	0.00	0.00	4.33	2.95	7.12	H2-K2	M27134
103371_at	0.00	0.00	0.00	2.62	3.44	2.54	UNK_AF100956	AF100956
102161_f_at	0.00	1.46	0.00	3.22	2.08	4.39	H2-Q2	X58609
98438_f_at	0.00	0.00	0.00	2.74	1.78	3.55	H2-Q7	X16202
93865_s_at	0.00	0.00	2.00	2.91	2.15	2.95	histocompatibility 2, T region locus 10,histocompatibility 2, T region locus 17,histocompatibility 2, T region locus 22,histocompatibility 2, T region locus 9; H2-T10,H2-T17,H2-T22,H2-T9	M35244

98472_at	0.00	0.00	2.30	3.40	2.50	4.96	H2-T23	Y00629
100708_at	0.00	0.00	0.00	2.88	2.50	2.60	H3 histone, family 3B; H3f3b	X13605
111734_at	0.00	0.00	0.00	3.21	3.18	4.05	UNK_AW121301	AW121301
104125_at	0.00	0.00	0.00	2.35	1.70	1.64	HA1R-PENDING	AA763673
92580_at	0.00	0.00	0.00	2.68	0.00	0.00	histidyl tRNA synthetase; Hars	U39473
98865_at	0.00	2.65	0.00	3.33	3.29	0.00	hyaluronan synthase 2; Has2	U52524
105550_at	0.00	1.93	2.61	2.31	2.78	0.00	HAS2	AI122156
103286_at	0.00	0.00	0.00	2.02	3.13	0.00	UNK_AB012611	AB012611
93483_at	2.86	5.24	2.12	3.21	10.07	3.83	hemopoietic cell kinase; Hck	J03023
99461_at	1.98	5.10	3.27	2.70	2.63	0.00	hematopoietic cell specific Lyn substrate 1; Hcls1	X84797
102851_s_at	0.00	2.75	5.77	5.45	2.90	4.43	HCPH	M68902
96046_at	0.00	0.00	0.00	2.52	1.79	0.00	HDAC1	X98207
92730_at	0.00	0.00	0.00	2.16	0.00	0.00	epidermal growth factor-like growth factor; Hegfl	L07264
97334_at	0.00	1.95	0.00	0.00	4.41	0.00	HES6	AW048812
94840_at	0.00	0.00	0.00	2.49	2.45	7.00	Hexa	U05837
101913_at	0.00	2.34	0.00	3.35	3.35	1.98	HEY1	AW214298
98628_f_at	0.00	1.91	0.00	3.83	3.98	3.08	factor 1, alpha subunit; Hif1a	AF003695
98629_f_at	0.00	1.97	0.00	3.82	3.68	3.30	HIF1A	Y09085
93250_r_at	0.00	4.01	0.00	7.33	4.74	4.32	HMG2	X67668
104285_at	0.00	0.00	0.00	0.00	4.78	0.00	methylglutaryl-Coenzyme A reductase; Hmgcr	M62766
96699_at	0.00	1.71	1.85	3.26	3.43	2.91	high mobility group protein 14; Hmg14	X53476
101589_at	0.00	2.37	2.80	4.52	3.86	3.35	high mobility group protein 17; Hmg17	X12944
93276_at	0.00	1.63	2.23	2.32	2.69	2.00	neurological expressed sequence 1; Hn1	U90123
97272_at	0.00	1.75	2.19	3.44	4.86	3.11	HNRPA1	M99167
94303_at	0.00	0.57	2.05	0.00	1.69	3.51	nuclear ribonucleoprotein D; Hnrpd	U11274
101485_at	0.00	0.00	0.00	5.33	3.02	2.04	HNRPDL	AW124859
93990_at	0.00	0.00	0.00	2.21	1.76	1.61	0	Y14196
95232_at	0.00	0.00	0.00	1.94	1.75	2.79	HNRPL	AB009392
96092_at	0.00	5.71	8.04	13.88	15.44	15.06	haptoglobin; Hp	M96827
93351_at	0.00	0.00	0.00	0.00	4.99	7.54	hydroxyprostaglandin dehydrogenase 15 (NAD); Hpgd	U44389
102306_at	0.00	0.00	0.00	3.65	4.58	3.02	HS2ST1	AF060178
101962_at	0.00	0.00	0.00	0.00	1.86	2.30	HSC70	AI854884
97261_at	0.00	1.77	0.00	0.00	2.16	2.28	HSJ2	AF055664
100353_g_at	0.00	2.82	0.00	0.00	2.79	0.00	HSPA4	AA919208
99816_at	0.00	0.00	0.00	0.00	2.43	0.00	heat shock protein, 70 kDa 2; Hsp70-2	M20567
95282_at	0.00	2.04	0.00	2.82	1.71	1.47	heat shock protein, 86 kDa 1; Hsp86-1	J04633
101955_at	0.00	1.92	1.98	3.00	2.30	1.78	GRP78	AJ002387
96254_at	0.00	1.99	0.00	0.00	3.44	3.03	HSPF1	AB028272

101399_at	0.00	0.00	0.00	0.00	2.72	0.00	perlecan (heparan sulfate proteoglycan 2); Hspg2	M77174
94236_at	0.00	0.00	0.00	0.00	2.44	1.97	UNK_AI838152	AI838152
100476_at	0.00	0.00	0.00	0.82	135.39	85.11	IBSP	L20232
100050_at	2.63	14.09	11.54	10.70	4.20	6.22	inhibitor of DNA binding 1; Idb1	M31885
92614_at	4.55	9.82	5.87	7.78	9.53	9.08	inhibitor of DNA binding 3; Idb3	M60523
99109_at	0.00	0.00	0.00	3.13	2.22	1.86	immediate early response 2; Ier2	M59821
94384_at	0.00	1.56	0.00	3.55	1.73	2.13	immediate early response 3; Ier3	X67644
92251_f_at	0.00	1.84	2.88	3.49	2.71	3.51	UNK_AA960657	AA960657
94224_s_at	0.00	2.12	3.85	3.55	2.35	2.62	UNK_M74123	M74123
98465_f_at	0.00	2.15	4.38	5.23	3.24	3.50	interferon activated gene 204; Ifi204	M31419
104750_at	0.00	3.40	7.66	4.69	2.10	4.67	interferon gamma inducible protein, 47 kDa; Ifi47	M63630
100981_at	0.00	0.00	8.75	0.00	3.37	2.08	interferon-induced protein with tetratricopeptide repeats 1; Ifit1	U43084
112340_at	0.00	0.00	4.49	1.51	0.00	0.00	UNK_AA178653	AA178653
103639_at	0.00	0.00	4.82	7.01	2.67	2.35	interferon-induced protein with tetratricopeptide repeats 2; Ifit2	U43085
93956_at	0.00	0.00	4.25	6.35	0.00	0.00	IFIT3	U43086
100483_at	0.00	0.00	2.24	3.74	4.92	4.19	interferon (alpha and beta) receptor; Ifnar	M89641
101014_at	0.00	0.00	3.34	0.00	2.93	3.31	IFNAR2	Y09864
101015_s_at	0.00	2.18	1.84	1.70	3.80	5.13	IFNAR2	AF013486
100552_at	0.00	0.00	0.00	3.89	1.88	2.16	IFNGR	M28233
95546_g_at	0.00	0.00	0.00	3.10	6.23	5.82	insulin-like growth factor 1; Igf1	X04480
98623_g_at	0.00	0.00	0.00	0.00	3.20	2.42	IGF2	X71922
95082_at	0.00	0.00	0.00	0.00	2.92	4.18	IGFBP3	AI842277
95083_at	0.00	0.00	0.00	0.00	7.76	6.72	factor binding protein 3; Igfbp3	X81581
101571_g_at	0.00	0.00	0.00	3.58	7.05	8.40	IGFBP4	X76066
103949_at	0.00	0.00	0.00	0.00	3.03	0.00	Indian hedgehog homolog, (Drosophila); Ihh	X76291
101054_at	0.00	1.83	0.00	2.41	2.02	3.39	Ia-associated invariant chain; Ii	X00496
96764_at	-2.18	0.00	4.23	4.92	2.47	10.03	UNK_AJ007971	AJ007971
111615_at	0.00	0.00	0.00	0.00	3.13	0.00	IKBKB	AW209118
99491_at	0.00	2.16	1.76	1.96	3.49	3.19	interleukin 10 receptor, beta; Il10rb	U53696
99991_at	0.00	2.79	0.00	0.00	1.72	3.32	interleukin 17 receptor; Il17r	U31993
103486_at	0.63	2.39	2.75	3.67	2.17	4.47	Il1b	M15131
93914_at	0.00	4.38	0.00	3.94	3.09	3.44	interleukin 1 receptor, type I; Il1r1	M20658
93871_at	0.00	0.00	0.00	4.89	1.33	3.75	IL1RN	L32838
102021_at	3.54	27.39	6.36	13.28	10.97	6.34	interleukin 4 receptor, alpha; Il4ra	M27960

102218_at	0.00	2.71	0.00	1.55	0.00	0.00	interleukin 6; Il6	X54542
101499_at	0.00	0.00	0.00	3.26	2.76	2.65	ILK	U94479
100277_at	0.00	0.00	2.28	5.04	4.35	0.00	inhibin beta-A; Inhba	X69619
94399_at	0.00	0.00	0.00	0.00	1.14	2.02	INPP5B	AI843172
102884_at	0.00	2.24	1.00	2.31	1.62	1.57	polyphosphate-5-phosphatase, 145 kDa; Inpp5d	U51742
100561_at	0.00	1.75	1.98	2.97	3.51	4.48	IQGAP1	AW209098
99103_at	0.00	0.00	0.00	0.00	2.24	0.00	IRF3	AF036341
93425_at	0.00	0.00	0.00	2.88	0.00	0.00	interferon regulatory factor 5; Irf5	AF028725
104669_at	0.00	0.00	1.37	2.31	3.90	2.76	interferon regulatory factor 7; Irf7	U73037
98822_at	1.83	2.50	7.89	17.45	7.07	5.85	protein (15 kDa); Isg15	X56602
103634_at	0.00	2.12	0.00	3.40	4.00	3.66	interferon dependent positive acting transcription factor 3 gamma; Isgf3g	U51992
99010_at	0.00	1.49	0.00	2.51	4.56	3.66	ISLR	AB024538
98366_at	0.00	0.00	0.00	0.00	2.16	3.20	integrin alpha V (Cd51); Itgav	U14135
100124_r_at	0.00	0.00	0.00	2.19	1.92	2.34	ITGB1	X15202
102353_at	1.84	2.21	2.43	2.51	3.29	7.22	ITGB2	M31039
94826_at	0.00	1.64	1.82	2.47	2.59	1.69	ITGB4BP	Y11460
100601_at	0.00	0.00	0.00	0.00	2.93	0.00	ITGB5	AF022110
103611_at	0.00	1.73	0.00	2.11	2.33	2.77	ITGP	AB012693
98922_at	0.00	0.00	0.00	0.00	2.69	2.27	intergral membrane protein 1; Itm1	L34260
93511_at	0.00	0.00	0.00	0.00	2.04	0.00	integral membrane protein 2; Itm2	L38971
96283_at	0.00	0.00	0.00	4.19	9.42	7.02	UNK_AI849180	AI849180
99509_s_at	0.00	0.00	0.00	0.00	6.28	0.00	JAK3	L40172
103816_at	0.00	0.00	0.00	1.96	1.74	2.64	JCAM	U89915
102362_i_at	2.25	5.90	2.20	8.24	4.87	0.00	Junb	U20735
102363_r_at	0.00	6.13	3.53	14.86	4.92	0.00	Junb	U20735
102364_at	0.00	0.00	0.00	0.00	2.24	2.09	JUND1	J04509
114683_at	0.00	0.00	0.00	0.00	2.12	4.85	KAP	AW125126
102892_at	0.00	2.18	0.00	0.00	1.30	1.61	KCNAB2	U65592
109931_at	0.00	0.00	0.00	0.00	4.27	2.96	UNK_AW214619	AW214619
102335_at	0.00	0.00	0.00	0.00	4.22	5.08	KCNK1	AF033017
104652_at	0.00	0.00	0.00	0.00	1.71	3.71	KCNK2	AI849601
102198_at	0.00	5.02	4.23	5.49	6.12	6.03	KCNN4	AF042487
102644_at	0.00	2.13	2.16	3.29	3.28	4.38	derived transcript 1; Kdt1	U13371
106026_at	0.00	0.00	0.00	2.22	1.11	0.00	KELCHL	AI845205
99541_at	0.00	0.00	2.42	2.19	2.31	1.50	KIFL1	AJ223293
94276_at	0.00	2.50	0.00	2.52	1.93	2.89	UNK_AF064635	AF064635
100010_at	0.00	0.00	0.00	0.00	2.38	2.04	Kruppel-like factor 3 (basic); Klf3	U36340
99622_at	0.00	0.00	0.00	0.00	2.46	2.79	Kruppel-like factor 4 (gut); Klf4	U20344
102707_f_at	0.00	0.00	3.80	0.00	0.00	0.00	kallikrein binding protein; Klkbp	X61597
93677_at	0.00	0.00	0.00	1.68	2.07	1.74	KLRD1	AF030311
92790_at	0.00	3.36	3.06	3.84	3.02	2.72	(importin) alpha 2; Kpna2	D55720

97991_at	0.00	2.56	0.00	0.00	2.22	0.00	Kirsten rat sarcoma oncogene 2, expressed; Kras2	X02452
97909_at	0.00	5.50	6.71	11.66	11.44	8.79	UNK_AI838080	AI838080
104587_at	0.00	0.00	0.00	3.06	4.57	4.63	Lama4	U69176
101948_at	0.00	0.00	0.00	2.83	5.29	1.96	LAMB1-1	X05212
140322_at	0.00	0.00	2.48	2.50	2.39	2.59	LAMP2	AW018326
100136_at	0.00	0.00	0.00	2.49	2.82	2.87	LAMP2	M32017
100012_at	0.00	2.03	3.10	3.09	4.43	8.86	associated protein transmembrane 5; Laptm5	U29539
93793_at	0.00	1.73	1.73	3.30	4.36	5.96	LASP1	AW122780
93930_at	0.00	0.00	0.00	1.83	4.32	4.37	LIM and SH3 protein 1; Lasp1	U58882
114629_at	0.00	0.68	2.63	3.49	1.80	2.04	UNK_AW124408	AW124408
102957_at	0.00	3.04	0.00	3.19	2.47	4.63	lymphocyte cytosolic protein 2; Lcp2	U20159
93682_at	0.00	0.00	0.00	0.00	2.02	1.93	LDB3	U89489
93797_g_at	0.00	2.55	1.84	3.48	3.05	2.86	TCFL1	AW123952
93798_at	0.00	2.67	0.00	3.36	3.02	3.32	TCFL1	AI839988
93600_at	0.00	1.83	2.22	2.93	3.37	4.78	LEPR	AJ011565
100431_at	0.00	0.00	0.00	0.00	4.53	5.21	leptin receptor; Lepr	U42467
95706_at	0.00	0.00	1.74	4.15	3.83	10.29	binding, soluble 3; Lgals3	X16834
103335_at	0.00	1.81	2.08	2.99	2.89	2.47	binding, soluble 9; Lgals9	U55060
104659_g_at	0.00	0.00	0.00	0.00	5.33	11.04	LIFR	D17444
104657_at	0.00	0.00	0.00	0.00	1.77	3.26	leukemia inhibitory factor receptor; Lifr	D26177
102123_at	0.00	0.00	0.00	3.18	1.67	3.11	UNK_Z31689	Z31689
98059_s_at	0.00	2.68	2.74	4.63	3.92	2.97	lamin A; Lmna	D49733
93666_at	0.00	0.00	0.00	0.00	2.00	0.00	LMO2	M64360
95069_at	0.00	0.00	0.00	0.00	3.14	2.18	UNK_AA940430	AA940430
98122_at	0.00	0.00	0.00	0.00	2.19	1.94	LMO4	AF074600
93939_at	0.00	0.00	0.00	0.00	3.16	1.74	LNK	U89993
93885_g_at	0.00	0.00	0.00	0.00	1.92	3.59	LOC53423	AB034693
94997_at	0.00	0.00	0.00	0.00	1.76	2.65	LOC53423	AF060883
101518_at	0.00	0.00	0.00	3.58	5.95	4.14	uterine protein; LOC55978	U38981
92569_f_at	0.00	0.00	2.09	2.56	2.98	0.00	LOC55989	AF053232
115414_at	0.00	2.55	0.00	2.70	0.00	0.00	UNK_AI849017	AI849017
104524_at	0.00	1.64	1.93	0.00	2.21	3.77	UNK_AI842825	AI842825
96260_at	0.00	0.00	1.44	2.63	2.92	3.01	UNK_AB021491	AB021491
116843_at	0.00	0.00	0.00	0.06	2.61	2.86	UNK_AW045920	AW045920
93753_at	0.00	1.85	1.80	3.48	2.78	4.85	UNK_AI852632	AI852632
109105_i_at	0.00	0.00	0.00	1.57	4.79	4.72	UNK_AW122202	AW122202
109106_f_at	0.00	0.00	0.00	2.28	2.86	1.89	UNK_AW122202	AW122202
111200_at	0.00	0.00	0.00	0.00	2.70	0.00	UNK_AA726446	AA726446
96139_at	0.00	0.00	0.00	0.00	6.31	0.00	UNK_AF001797	AF001797
113180_at	0.00	0.00	0.00	0.00	2.75	0.00	UNK_AW125855	AW125855
113101_f_at	0.00	0.00	0.00	0.00	2.07	0.00	UNK_AI644869	AI644869
113215_i_at	0.00	0.00	0.00	0.00	2.52	1.42	UNK_AI850449	AI850449
113231_at	0.00	0.00	0.00	2.09	2.43	2.31	UNK_AI854099	AI854099
111385_at	0.00	0.00	0.00	0.00	3.75	0.00	UNK_AA734127	AA734127
138455_at	0.00	0.00	0.00	4.25	4.54	7.46	UNK_AI847317	AI847317
107403_at	0.00	0.00	0.00	0.00	5.41	2.12	UNK_AW047735	AW047735
111239_at	0.00	0.00	0.00	1.67	3.73	1.58	UNK_AI428160	AI428160
100408_at	0.00	0.00	0.00	0.00	2.27	0.00	UNK_AA839465	AA839465
116332_at	0.00	0.00	0.00	0.00	2.64	0.00	UNK_AW228823	AW228823

111391_at	0.00	2.16	0.00	2.12	4.09	3.51	UNK_AI846729	AI846729
101073_at	0.00	0.00	0.00	1.86	1.89	2.07	low density lipoprotein receptor related protein; Lrp	X67469
92564_at	0.00	0.00	0.00	0.00	2.44	1.96	LRRFIP1	AI891475
104093_at	0.00	1.65	0.00	3.08	7.88	3.15	LSP1	D49691
103571_at	0.00	2.58	2.53	4.71	12.61	7.37	LST1	U72644
100540_at	0.00	0.00	0.00	1.94	2.39	2.10	leukotriene A4 hydrolase; Lta4h	M63848
103209_at	0.00	0.00	0.00	0.00	2.04	0.00	UNK_AF022889	AF022889
92335_at	2.27	5.35	4.42	7.37	8.46	3.49	growth factor beta binding protein 2; Ltbp2	AF004874
96090_g_at	0.00	0.00	0.00	0.00	1.48	2.59	UNK_AI255972	AI255972
93353_at	0.00	0.00	0.00	2.37	4.25	4.32	lumican; Lum	AF013262
96065_at	0.00	2.48	2.99	4.79	10.45	4.81	latexin; Lxn	D88769
114822_f_at	0.00	0.00	0.00	2.23	1.71	2.53	UNK_AA762251	AA762251
100771_at	0.00	2.32	0.00	3.22	2.64	0.00	LY57	AF068182
100772_g_at	0.00	0.00	0.00	3.32	3.38	0.00	LY57	AF068182
93078_at	0.00	0.00	0.00	2.01	0.00	0.00	LY6	X04653
101487_f_at	0.00	1.52	1.77	2.89	2.34	2.43	LY6E	U47737
94425_at	0.00	2.66	1.85	3.26	2.53	2.88	LY86	AB007599
100468_g_at	0.00	1.84	2.02	2.66	1.65	2.94	lymphoblastomic leukemia; Lyl1	X57687
100467_at	0.00	0.00	2.64	0.00	0.00	0.00	lymphoblastomic leukemia; Lyl1	X57687
103349_at	0.00	2.70	2.60	0.00	4.26	0.00	viral (v-yes-1) oncogene homolog; Lyn	M57696
101753_s_at	0.00	1.77	2.34	3.14	2.90	3.36	LZP-S	X51547
100477_at	0.00	3.23	0.00	7.39	9.49	5.76	hypothetical protein 19.5; p19.5	M32486
92847_s_at	0.00	1.93	1.57	3.01	1.89	3.90	M6PR	X56831
96865_at	0.00	0.00	1.70	2.61	3.59	3.60	alanine rich protein kinase C substrate; Macs	M60474
99632_at	0.00	3.64	3.71	5.79	4.99	3.29	MAD2L1	U83902
99024_at	0.00	0.00	0.00	2.37	3.96	3.22	Max dimerization protein 4; Mad4	U32395
102983_at	0.00	0.00	0.00	2.26	2.67	2.46	MADH1	U58992
102984_g_at	0.00	0.00	0.00	0.00	2.46	2.38	MADH1	U58992
104536_at	0.00	0.00	0.00	2.18	2.08	2.27	MADH2	U60530
104220_at	2.64	2.73	2.60	2.03	1.86	1.93	MADH6	AF010133
114338_at	0.00	2.06	2.77	3.20	3.21	4.58	MAFB	AI642664
102204_at	0.00	2.04	0.00	1.93	3.78	3.95	musculoaponeurotic fibrosarcoma oncogene family, protein B (avian); Mafb	L36435
117143_s_at	0.00	0.00	0.00	2.70	2.61	3.69	MAFB	AW213708
117144_r_at	0.00	0.00	0.00	0.00	4.02	3.31	MAFB	AW213708
105228_at	0.00	1.54	0.00	1.91	3.85	3.66	MAN1B	AI528764
110305_at	0.00	0.00	0.00	0.00	4.70	3.60	MAN1B	AA960561
104628_at	0.00	1.85	0.00	4.09	2.33	3.10	mannosidase 2, alpha 1; Man2a1	X61172
99562_at	0.00	2.00	2.50	3.15	3.16	4.31	MAN2B1	U87240
102195_at	0.00	0.00	2.76	2.19	2.65	3.58	protein kinase kinase kinase kinase 4; Map4k4	U88984

103416_at	0.00	0.00	0.00	2.14	1.55	1.98	MAPK6	AI844810
98475_at	0.00	0.00	0.00	3.59	8.68	5.06	matrilin 2; Matn2	U69262
102089_at	0.00	0.00	0.00	0.00	11.72	0.00	MATN3	Y10521
96835_at	0.00	0.00	0.00	0.00	23.39	8.68	MATN4	AJ010984
99095_at	0.00	0.00	0.00	1.82	2.24	2.47	Max protein; Max	M63903
96767_at	0.00	1.83	1.99	3.73	4.04	3.18	MBC2	AF098633
100062_at	0.00	2.91	3.11	3.83	3.44	2.47	maintenance deficient (S. cerevisiae); Mcmd	X62154
93112_at	0.00	0.00	1.92	0.00	2.36	0.00	MCMD2	D86725
93041_at	0.00	7.24	7.49	6.58	4.25	2.16	maintenance deficient 4 homolog (S. cerevisiae); Mcmd4	D26089
100156_at	0.00	7.39	9.72	7.89	7.48	2.57	maintenance deficient 5 (S. cerevisiae); Mcmd5	D26090
93356_at	0.00	0.00	0.00	0.00	2.28	2.63	maintenance deficient 7 (S. cerevisiae); Mcmd7	D26091
99133_at	0.00	2.08	1.76	3.23	3.10	2.32	monoclonal antibodies 4F2; Mdu1	X14309
103584_at	0.00	2.17	2.27	3.29	4.01	4.66	UNK_AW124334	AW124334
92607_at	0.00	0.00	0.00	4.80	35.79	13.98	MEST	AF017994
101095_at	0.00	0.00	0.00	0.00	7.21	12.75	associated protein 2; Mfap2	L23769
131248_at	1.92	0.00	0.00	2.86	4.34	2.62	MFAP5-PENDING	AI608002
99518_at	1.91	0.00	0.00	2.66	2.54	1.97	MFAP5-PENDING	AW121179
92880_at	0.00	0.00	0.00	0.00	2.78	1.95	factor 8 protein; Mfge8	M38337
103080_at	0.00	2.28	3.11	3.79	2.29	3.86	IFN-gamma induced; Mg11	U15635
110672_at	0.00	0.00	0.00	2.18	0.00	0.00	MGL	AW049068
93866_s_at	0.00	0.00	0.00	0.00	2.01	2.44	matrix gamma-carboxyglutamate (gla) protein; Mglap	D00613
104410_at	0.00	0.00	0.00	3.62	2.31	2.44	UNK_AW124785	AW124785
99457_at	0.00	4.86	5.97	6.25	6.68	4.02	antigen identified by monoclonal antibody Ki 67; Mki67	X82786
101069_g_at	0.00	1.70	0.00	0.00	2.03	3.10	MKRN1	AA656621
97203_at	0.00	4.21	3.45	4.84	7.71	7.84	MLP	X61399
92331_at	0.00	0.00	0.00	0.00	5.67	3.92	endopeptidase; Mme	M81591
98280_at	0.00	0.00	0.00	0.00	1.80	2.98	UNK_AB021228	AB021228
112880_at	0.00	0.00	0.00	2.93	7.30	4.28	MMP23	AA144420
98833_at	0.00	0.00	0.00	0.00	0.53	2.49	metalloproteinase 3; Mmp3	X66402
99957_at	0.00	0.00	0.00	39.03	26.93	96.46	MMP9	X72795
95045_at	0.00	1.45	0.00	3.50	3.07	2.57	UNK_AI844469	AI844469
131220_f_at	0.00	0.00	0.00	0.00	2.24	0.00	UNK_AW123699	AW123699
95951_at	0.00	3.67	2.20	3.26	2.12	1.72	MPCL	AF061272
99071_at	0.00	1.53	2.18	3.44	4.43	9.63	expressed gene 1; Mpeg1	L20315
94857_at	0.00	0.00	0.00	0.00	2.55	2.53	N-methylpurine-DNA glycosylase; Mpg	U10420

97803_at	0.00	2.84	3.15	3.77	2.11	3.63	membrane protein, palmitoylated (55 kDa); Mpp1	U38196
103226_at	3.09	5.30	3.98	3.64	2.84	2.41	mannose receptor, C type 1; Mrc1	Z11974
100759_at	0.00	0.00	0.00	0.00	7.71	3.67	mannose receptor, C type 2; Mrc2	U56734
96633_s_at	0.00	0.00	0.00	2.25	2.20	2.01	Sid393p; Sid393p	AA529583
96632_at	0.00	0.00	0.00	2.23	1.96	1.69	UNK_AB025049	AB025049
96120_at	0.00	0.00	0.00	2.06	1.64	1.99	MRJ-PENDING	AW124750
98373_at	0.00	2.29	3.59	2.69	0.00	0.00	UNK_AI462516	AI462516
93234_at	0.00	0.00	0.00	0.00	3.55	0.00	MSC	AF087035
93602_at	0.00	2.16	0.00	0.00	3.26	2.23	UNK_AF074714	AF074714
93573_at	0.00	2.93	2.31	8.18	4.56	10.01	Mt1	V00835
101561_at	0.00	2.89	2.70	5.96	4.03	7.42	Mt2	K02236
108780_at	0.00	2.32	2.52	3.20	4.77	3.11	UNK_AI845395	AI845395
100046_at	0.00	0.00	3.84	6.20	4.36	3.26	folate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate	J04627
98417_at	2.13	0.00	2.31	2.78	1.96	1.90	MX1	M21038
96285_at	0.00	1.55	1.71	3.13	2.84	2.61	MYADM	AJ001616
104712_at	0.00	2.70	2.99	2.96	4.49	2.41	myelocytomatosis oncogene; Myc	L00039
102430_at	0.00	4.68	0.00	4.96	6.64	4.14	differentiation primary response gene 88; Myd88	X51397
106557_at	0.00	0.00	0.00	3.15	5.61	4.03	UNK_AI132668	AI132668
100923_at	0.00	0.00	0.00	0.00	1.80	2.22	MYO10	AJ249706
98409_at	0.00	0.00	1.41	2.83	7.66	9.17	myosin Ib; Myo1b	L00923
95506_at	0.00	0.00	0.00	0.00	2.37	0.00	MYO1C	U96723
101708_at	0.00	0.00	0.00	0.00	1.61	2.32	myosin If; Myo1f	X97650
98968_at	0.00	1.84	2.19	1.68	1.71	2.15	myosin Va; Myo5a	X57377
94713_at	0.00	0.00	0.00	0.00	2.66	4.15	myosin VIIa; Myo7a	U81453
114776_at	0.00	0.00	0.00	3.11	8.64	5.61	MYO9B	AA739159
102986_at	3.53	3.84	2.32	2.76	2.31	0.00	MYOD1	M18779
103053_at	0.00	3.08	0.00	8.00	4.91	0.00	MYOG	X15784
94408_at	0.00	0.00	0.00	2.01	2.30	3.18	Ngfi-A binding protein 1; Nab1	U47008
100962_at	0.00	0.00	1.99	2.66	3.48	3.63	Ngfi-A binding protein 2; Nab2	U47543
103637_at	0.00	0.00	0.00	0.00	4.22	4.03	NAGA	AJ223966
93373_at	0.00	0.00	0.00	0.00	3.21	6.08	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Naglu	U85247
98587_at	0.00	1.60	2.17	2.65	2.40	1.80	assembly protein 1-like 1; Nap1l1	X61449
101108_at	0.00	4.08	0.00	0.00	0.00	0.00	autoantigenic sperm protein (histone-binding); Nasp	AF034610
100153_at	0.00	0.00	1.32	4.10	4.06	2.79	neural cell adhesion molecule; Ncam	X15052
99633_at	0.00	0.00	0.00	0.00	2.26	0.00	NCDN-PENDING	AB017608
102326_at	0.00	4.13	0.00	0.00	1.95	2.92	NCF2	AB002664
100144_at	0.00	0.00	0.00	2.36	2.06	0.00	nucleolin; Ncl	X07699
94047_at	0.00	1.49	0.00	2.17	2.44	3.23	UNK_AW122935	AW122935
101059_at	0.00	0.00	0.00	2.49	2.14	0.00	NDN	D76440

100472_at	0.00	0.00	0.00	3.04	2.49	1.99	NPC derived proline rich protein 1; Ndpp1	D10727
107467_at	0.00	0.00	0.00	2.05	2.13	1.80	UNK_AW047444	AW047444
92518_at	0.00	0.00	0.00	0.00	2.48	0.00	NEO1	Y09535
103549_at	0.00	0.00	0.00	1.88	2.33	0.00	NES	AW061260
115217_at	0.00	0.00	0.00	0.00	2.02	3.11	NFAT5	AI852272
102209_at	0.00	0.00	3.02	6.06	3.92	12.16	NFATC1	AF087434
115215_at	0.00	0.00	0.00	5.96	7.00	13.80	UNK_AA638441	AA638441
98427_s_at	0.00	0.00	0.00	2.48	1.83	2.18	NFKB1	M57999
100469_at	0.00	0.00	0.00	2.00	2.53	3.49	NFYA	D78642
93563_s_at	0.00	2.18	3.71	4.33	5.30	3.48	NID2	AB017202
93318_at	0.00	0.00	3.63	0.00	1.52	0.00	NINJ1	U91513
92794_f_at	0.00	0.00	1.84	0.00	2.49	1.46	NME1	M35970
102047_at	0.00	0.00	0.00	2.17	0.00	0.00	NMT1	AF043326
101473_at	0.00	0.00	0.00	0.00	7.66	5.81	NNMT	U86108
104132_at	0.00	0.00	0.00	2.32	3.69	0.00	NOC4	AW047276
106115_at	0.00	0.00	0.00	2.39	2.08	0.00	UNK_AI849335	AI849335
102028_at	0.00	0.00	0.00	4.05	2.85	3.43	NORE1	AF053959
100507_at	0.00	0.00	0.00	2.01	4.45	6.67	nephroblastoma overexpressed gene; Nov	Y09257
114812_at	0.00	0.00	0.00	2.08	6.43	3.89	UNK_AA869278	AA869278
99564_at	0.00	3.62	3.98	4.26	2.21	2.67	NP95	D87908
92626_at	0.00	0.00	0.00	3.12	3.55	2.70	differentiation and control gene 1; Npdc1	X67209
101634_at	0.00	0.00	1.77	2.55	2.14	0.00	Npm1	M33212
102796_at	0.00	3.11	0.00	0.00	0.00	0.00	Npm3	U64450
101168_at	0.00	0.00	0.00	2.07	2.52	1.94	neoplastic progression 1; Npn1	Z31360
93202_at	0.00	0.00	0.00	0.00	2.18	1.62	5' nucleotidase; Nt5	L12059
96666_at	0.00	0.00	0.00	0.00	4.20	0.00	N-terminal Asn amidase; Ntan1	U57692
94528_at	1.73	3.32	1.59	1.72	1.90	0.00	NUBP1	AI846206
94839_at	0.00	0.00	0.00	2.37	2.60	2.29	nucleobindin; Nucb	M96823
102197_at	0.00	0.00	0.00	2.38	3.20	2.50	NUCB2	AJ222586
101593_at	0.00	0.00	0.00	0.00	3.55	0.00	UNK_AI851454	AI851454
108579_at	0.00	2.97	0.00	2.53	5.55	2.93	NUDT5	AI854177
93046_at	0.00	0.00	0.00	0.00	3.03	1.95	UNK_AW045233	AW045233
102231_at	0.00	0.00	0.00	0.00	7.53	3.00	OASIS-PENDING	AB017614
107525_at	0.00	2.46	5.90	6.26	4.94	5.61	OASL	AW211637
101002_at	0.00	2.02	0.00	2.36	1.89	1.67	decarboxylase antizyme inhibitor;	AF032128
99549_at	0.00	-3.17	0.00	0.00	3.34	2.12	osteoglycin; Ogn	D31951
93369_at	0.00	0.00	0.00	0.00	9.11	5.81	osteomodulin; Omd	AB007848
95712_at	0.00	2.64	0.00	3.22	2.28	1.84	UNK_AW045261	AW045261
96093_at	0.00	0.00	0.00	3.36	0.00	0.00	UNK_AI842705	AI842705
117253_at	0.00	0.00	0.00	1.90	3.19	0.00	UNK_AI845729	AI845729
100437_g_at	0.00	0.00	0.00	3.83	0.00	0.00	Orm1	M27008
92593_at	2.42	2.26	4.11	5.43	13.56	19.79	osteoblast specific factor 2; OSF-2	D13664
102255_at	0.00	0.00	0.00	3.29	2.68	3.26	OSMR	AB015978
100138_f_at	0.00	1.82	2.20	0.00	2.88	0.00	similar to human SYK interacting protein; p16K	X52102
95586_at	0.00	0.00	3.82	3.90	3.26	1.84	P2RX4	AF089751
96016_at	0.00	2.47	0.00	6.19	4.91	2.57	P40-8	AW045665

104139_at	0.00	0.00	0.00	1.90	2.21	1.82	2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide; P4ha1	U16162
98983_at	0.00	0.00	0.00	2.64	5.05	2.80	2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide; P4ha2	U16163
100720_at	0.00	1.59	2.28	2.36	3.73	2.53	protein, cytoplasmic 1; Pabpc1	X65553
98021_at	0.00	0.00	0.00	0.00	2.39	0.00	0	D14336
99023_at	0.00	1.65	0.00	4.28	2.73	0.00	factor acetylhydrolase, isoform 1b, alpha2 subunit; Pafah1b2	U57747
100576_at	0.00	0.00	0.00	1.95	2.29	2.64	factor acetylhydrolase, isoform 1b, alpha1 subunit; Pafah1b3	U57746
114355_at	0.00	0.00	2.27	5.58	4.79	0.00	PANX1	AI847747
93298_at	0.00	0.00	0.00	0.00	3.57	3.43	phosphoadenosine 5'-phosphosulfate synthase 1; Papss1	U34883
96713_at	0.00	0.00	0.00	0.00	5.09	4.94	PAPSS2	AF052453
93615_at	0.00	1.75	0.00	2.33	2.68	2.35	pre B-cell leukemia transcription factor 3; Pbx3	AF020200
94449_at	0.00	0.00	0.00	0.00	2.50	3.46	PCDH13	AI854522
102280_at	0.00	0.00	0.00	0.00	1.82	3.45	PCDH7	AB006758
102781_at	0.00	0.00	0.00	0.00	2.31	2.76	enhanced expression; PCEE	U37351
109761_g_at	0.00	0.00	0.00	2.91	5.10	0.00	UNK_AI848972	AI848972
101065_at	0.00	3.07	2.87	3.72	2.58	2.41	PCNA	X57800
93349_at	0.00	0.00	0.00	3.50	6.60	6.15	proteinase enhancer protein; Pcolce	X57337
92192_s_at	0.00	0.00	2.04	3.28	4.63	2.79	PCSK5	D12619
101196_at	0.00	0.00	0.00	0.00	2.74	3.02	convertase subtilisin/kexin type 6; Pcsk6	D50060
95412_at	0.00	0.00	0.00	2.35	2.36	2.10	programmed cell death 6; Pdcd6	U49112
96252_at	0.00	1.55	0.00	2.17	2.00	1.80	PDCD6IP	AJ005073
93382_at	0.00	0.00	0.00	0.00	2.51	0.00	PDE1B1	AF023343
116964_at	0.00	0.00	0.00	6.04	14.08	9.38	UNK_AI851805	AI851805
93574_at	0.00	0.00	1.71	3.31	3.42	4.08	SDF3	AF036164
115553_at	0.00	0.00	2.11	2.15	0.00	0.00	UNK_AI841779	AI841779
101451_at	0.00	0.00	0.00	2.15	2.01	3.16	PEG3	AF038939
96765_at	0.00	0.00	0.00	2.41	2.67	1.76	PEG3	AW120874
94516_f_at	0.00	0.00	0.00	0.00	5.97	3.99	PENK2	M55181
101468_at	2.20	3.94	4.04	4.10	3.07	1.92	properdin factor, complement; Pfc	X12905
97834_g_at	0.00	2.07	2.29	3.11	2.38	2.29	UNK_AI853802	AI853802
97833_at	0.00	0.00	0.00	2.77	2.41	0.00	UNK_AI853802	AI853802
93421_at	0.00	3.19	0.00	3.98	5.66	4.45	PFTAIRE protein kinase 1; Pftk1	AF033655
101585_at	0.00	0.00	2.28	2.71	5.13	6.27	PGRMC-PENDING	AF042491
94406_at	0.00	0.00	0.00	0.00	6.01	4.58	PHTF	AJ242864

93708_at	0.00	0.00	0.00	0.00	2.16	1.78	PIAS3	AF034080
92312_at	0.00	0.00	0.00	0.00	3.14	0.00	PIK3C2A	U55772
96592_at	0.00	0.00	1.93	0.00	2.15	2.21	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha); Pik3r1	U50413
101926_at	0.00	0.00	0.00	0.00	2.74	0.00	proviral integration site 2; Pim2	L41495
95358_at	0.00	0.00	0.00	1.63	1.80	2.05	UNK_AI843864	AI843864
100328_s_at	4.40	8.50	5.17	12.16	2.38	11.48	PIRA3	U96684
98003_at	0.00	2.48	0.00	3.55	3.42	3.45	PIRB	AF038149
102696_s_at	0.00	0.00	2.49	0.00	2.01	2.44	UNK_AI747899	AI747899
101461_f_at	0.00	0.00	0.00	2.09	2.39	2.19	PJA1	U06944
104531_at	0.00	1.31	1.42	1.63	2.40	2.42	protein kinase C, delta; Pkcd	X60304
97375_at	0.00	0.00	0.00	0.00	2.90	3.20	disease 1 homolog; Pkd1	U70209
100951_at	0.00	0.00	0.00	2.13	3.19	3.22	polycystic kidney disease 2; Pkd2	AF014010
99513_at	1.58	5.00	0.00	10.15	10.27	5.24	phospholipase A2, group 4; Pla2g4	M72394
94147_at	4.28	9.58	8.85	11.13	4.61	4.14	activator inhibitor, type I; Planh1	M33960
102663_at	0.00	0.00	0.00	5.52	8.24	0.00	PLAUR	X62700
104580_at	0.00	0.00	0.00	0.00	13.32	9.79	UNK_U85711	U85711
100607_at	0.00	0.00	6.30	10.02	22.31	16.77	Pld3	AF026124
112083_at	0.00	3.60	4.03	3.29	3.72	4.57	PLEK	AA389905
116483_at	0.00	2.51	0.00	1.45	1.58	1.45	PLEK	AA178053
93099_f_at	0.00	0.00	5.64	0.00	7.14	0.00	homolog, (Drosophila); Plk	U01063
101350_g_at	0.00	0.00	0.00	2.69	3.15	0.00	PLK-PS1	U73170
112304_at	0.00	0.00	0.00	2.53	2.40	3.41	PLOD1	AI854890
114376_at	0.00	0.00	0.00	10.32	19.49	16.29	PLOD2	AW259579
95009_at	0.00	0.00	0.00	3.52	2.66	0.00	PLOD3	AW107836
108848_g_at	0.00	2.15	2.34	3.50	3.60	3.50	UNK_AW261779	AW261779
93323_at	0.00	1.77	1.99	4.35	4.15	3.14	UNK_AB031292	AB031292
94278_at	2.52	5.35	7.31	6.59	8.70	23.61	plastin 2, L; Pls2	D37837
102839_at	0.00	0.00	0.00	0.00	2.71	0.00	scramblase 1; Plscr1	D78354
100927_at	0.00	1.61	2.29	3.88	3.87	3.35	PLTP	U28960
97900_at	0.00	0.00	0.00	2.38	0.00	0.00	PLUNC	AI845714
93290_at	0.00	3.58	4.71	4.54	4.00	4.14	PNP	U35374
103207_at	0.00	0.00	0.00	1.97	2.15	1.44	POLA1	D13543
93940_at	0.00	0.00	0.00	0.00	2.74	2.18	Pon3	L76193
98508_s_at	0.00	0.00	0.00	2.11	1.67	1.47	PPAP2A	D84376
109095_at	0.00	0.00	0.00	0.00	1.61	4.80	PPAP2C	AI837099
101055_at	0.00	0.00	0.00	1.90	2.19	4.26	beta-galactosidase; Ppgb	J05261
101207_at	0.00	1.60	1.73	2.43	2.37	2.22	peptidylprolyl isomerase A; Ppia	X52803
94915_at	0.00	2.15	2.53	4.59	5.13	5.64	PPIB	X58990
100089_at	0.00	0.00	0.00	2.99	6.25	8.51	peptidylprolyl isomerase C; Ppic	M74227
97507_at	0.00	1.87	3.36	5.70	2.90	4.09	isomerase C-associated protein; Ppicap	X67809

98993_at	0.00	2.04	0.00	3.07	3.11	3.12	protein phosphatase 2, regulatory subunit B (B56), gamma isoform; Ppp2r5c	U59418
95631_at	0.00	1.74	1.72	2.71	2.96	2.24	UNK_AF088911	AF088911
93495_at	0.00	3.41	3.81	6.33	10.88	6.68	Prdx4	U96746
95549_at	0.00	0.00	0.00	0.00	2.83	0.00	PRIM2	D13545
100684_at	0.00	0.00	1.65	2.87	2.86	2.56	substrate 80K-H; Prkcsh	U92794
102414_i_at	0.00	1.63	1.80	2.44	2.02	1.69	interferon inducible double stranded RNA dependent inhibitor; Prkri	U28423
102415_r_at	0.00	0.00	0.00	0.00	2.50	0.00	interferon inducible double stranded RNA dependent inhibitor; Prkri	U28423
104728_at	0.00	2.54	0.00	3.40	4.10	4.80	Pros1	L27439
103327_at	3.94	5.14	4.58	8.52	7.86	5.35	paired related homeobox 2; Prrx2	X52875
93261_at	***0.00***	***3.35***	***4.35***	***6.68***	***5.66***	***3.99***	***PRSC1***	***AJ000990***
96920_at	0.00	-1.76	0.00	0.00	3.99	3.39	PRSS11	AW125478
104102_at	0.00	0.00	0.00	0.00	5.09	0.00	UNK_AW047978	AW047978
103433_at	0.00	0.00	0.00	0.00	2.56	2.17	PSCD3	AI846077
102791_at	0.00	2.23	2.86	4.09	2.59	4.48	PSMB8	U22033
100588_at	0.00	0.00	0.00	2.43	1.91	2.49	PSME2	U60329
103946_at	0.00	3.04	0.00	5.29	5.18	14.26	threonine phosphatase-interacting protein 1;	U87814
102105_f_at	0.00	0.00	0.00	0.00	3.33	0.00	PTGDS	AI840733
103362_at	0.00	1.42	0.00	1.93	3.68	0.00	receptor EP4 subtype; Ptgerep4	D13458
104406_at	0.00	0.00	0.00	0.00	3.15	1.63	UNK_AI060798	AI060798
104538_at	0.00	0.00	0.00	0.00	8.77	10.57	prostaglandin I2 (prostacyclin) synthase; Ptgis	AB001607
104647_at	1.32	4.33	7.11	10.53	8.79	1.69	prostaglandin-endoperoxide synthase 2; Ptgs2	M88242
98482_at	0.00	0.00	0.00	4.76	34.85	20.48	PTHR	X78936
93646_at	0.00	1.74	0.00	0.00	4.58	2.84	PTK9	U82324
100718_at	0.00	2.16	2.29	3.42	3.73	4.16	Ptma	X56135
96426_at	0.00	1.32	1.37	1.69	2.19	1.80	PTMB4	U38967
97474_r_at	0.00	0.00	0.00	0.00	2.93	1.82	pleiotrophin; Ptn	D90225
94929_at	0.00	2.13	0.00	2.61	2.81	4.92	PTPN1	M97590
98424_at	0.00	0.00	0.00	0.00	3.23	7.57	PTPN13	D83966
92273_at	1.97	3.65	0.00	3.39	0.00	0.00	PTPN18	U49853
101996_at	0.00	1.60	0.00	0.00	2.29	1.61	PTPN2	M80739
100976_at	0.00	2.38	0.00	3.41	4.06	2.87	protein-tyrosine phosphatase; Ptpn9	AF013490
103070_at	0.00	3.60	4.76	6.60	10.28	10.14	PTPNS1	AB018194
100908_at	0.00	0.00	0.00	2.22	6.03	10.00	phosphatase, receptor type, A; Ptpra	M36033
101048_at	0.00	2.63	0.00	4.79	2.56	4.70	phosphatase, receptor type, C; Ptprc	M14343
101298_g_at	0.00	3.11	0.00	0.00	1.43	2.85	PTPRC	M23158

93896_at	0.00	0.00	0.00	0.00	5.11	6.76	phosphatase, receptor type, D; Ptprd	D13903
100427_at	0.00	2.56	2.33	2.28	1.23	2.61	phosphatase, receptor type, O; Ptpro	U37465
92731_at	3.07	17.44	6.55	6.96	5.75	0.00	pentaxin related gene; Ptx3	X83601
96719_i_at	0.00	0.00	0.00	0.00	2.58	0.00	parvalbumin; Pva	X59382
97415_at	0.00	0.00	0.00	0.00	3.23	4.63	RAS oncogene family; Rab3d	M89777
103579_at	0.00	1.69	0.00	0.00	1.72	5.55	RAS-related C3 botulinum substrate 2; Rac2	X53247
97319_at	0.00	3.34	3.30	9.39	11.41	5.14	UNK_AF084466	AF084466
96104_at	0.00	0.00	0.00	2.14	2.20	3.10	RAD23B	AI047107
104527_at	0.00	0.00	2.19	2.89	2.79	0.00	RAD51	D13803
93676_at	0.00	0.00	0.00	0.00	2.01	0.00	RAD51AP1	U93583
102649_s_at	0.00	2.14	0.00	2.23	2.22	1.59	RAET1C	D64162
106071_at	0.00	5.58	0.00	6.56	5.61	3.57	RALY	AI852199
103299_at	1.92	0.00	2.97	3.91	4.13	3.15	UNK_AW123773	AW123773
114344_at	0.00	0.00	0.00	2.22	3.25	3.57	UNK_AA882453	AA882453
101254_at	0.00	0.00	0.00	2.17	0.00	0.00	oncogene family; Ran	L32751
98573_r_at	0.00	2.30	2.42	3.53	2.49	2.60	RAN binding protein 1; Ranbp1	X56045
93319_at	0.00	1.64	2.16	2.61	4.49	5.27	RAS p21 protein activator 3; Rasa3	U20238
102821_s_at	0.00	0.00	0.00	2.31	0.00	0.00	RAS-like, family 2, locus 9; Rasl2-9	L32752
102379_at	0.00	3.37	2.64	3.54	0.00	0.00	UNK_AW049415	AW049415
104476_at	0.00	0.00	0.00	2.96	2.77	2.03	retinoblastoma-like 1 (p107); Rbl1	U27177
96041_at	0.00	2.15	2.72	3.76	2.78	2.42	RBM3	AB016424
97254_at	0.00	0.00	0.00	2.49	1.83	0.00	UNK_AA690061	AA690061
94972_at	0.00	0.00	0.00	0.00	3.12	0.00	UNK_AB026569	AB026569
97847_at	0.00	0.00	0.00	0.00	4.07	0.00	RBMX	AJ237847
104716_at	0.00	0.00	0.00	3.52	4.52	2.49	protein 1, cellular; Rbp1	X60367
96047_at	0.00	0.00	0.00	0.00	3.29	3.03	protein 4, plasma; Rbp4	U63146
103804_at	0.00	0.00	0.00	0.00	3.42	2.10	ST15	AB006960
102960_at	0.00	0.00	0.00	2.03	2.18	2.31	recombination activating gene 1 gene activation; Rga	X96618
94378_at	0.00	0.00	0.00	0.00	3.49	0.00	protein signaling 16; Rgs16	U94828
94899_at	0.00	0.00	0.00	0.00	2.08	2.09	protein 3; Rhoip3-pending	U73200
104094_at	0.00	0.00	0.00	0.00	2.15	0.00	LIM gene; Ril-pending	Y08361
114018_at	0.00	2.49	1.95	4.66	6.14	0.00	UNK_AI504675	AI504675
97091_at	0.00	0.00	0.00	0.00	3.11	2.05	interacting serine-threonine kinase 1; Ripk1	U25995
96038_at	0.00	1.76	0.00	2.90	2.58	2.66	UNK_AI840339	AI840339
93164_at	0.00	0.00	0.00	0.00	2.18	2.16	ring finger protein 2; Rnf2	Y12783
93782_at	0.00	1.68	1.84	3.36	3.67	3.28	RNF4	AI844517

93453_at	0.00	0.00	0.00	0.00	2.62	0.00	rod outer segment membrane protein 1; Rom1	M96760
100711_at	0.00	0.00	0.00	2.10	1.93	0.00	ribosomal protein L10A; Rpl10a	U12403
92834_at	0.00	2.71	3.10	4.50	4.86	3.15	ribosomal protein L13a; Rpl13a	X51528
94208_at	0.00	2.29	3.47	4.81	4.93	2.77	RPL27A	AW045202
94209_g_at	0.00	2.19	4.15	3.80	4.81	2.50	RPL27A	AW045202
94207_at	0.00	2.31	2.67	4.56	2.55	0.00	RPL27A	AI842377
95418_at	0.00	0.00	0.00	0.00	2.52	0.00	UNK_AI848851	AI848851
100734_at	0.00	2.31	2.75	3.97	3.44	4.20	ribosomal protein L3; Rpl3	Y00225
108097_at	0.00	0.00	0.00	0.00	2.70	4.31	UNK_AW121237	AW121237
99624_at	0.00	0.00	0.00	2.07	2.20	2.07	UNK_AW125517	AW125517
92325_at	0.00	0.00	0.00	0.00	3.50	2.79	RPL7A	AI326889
96295_at	0.00	2.06	2.94	4.52	9.84	5.38	RPMS7	AW122030
94076_i_at	0.00	1.53	1.91	3.06	2.69	2.95	ribophorin; Rpn	D31717
94077_f_at	0.00	0.00	0.00	2.44	2.46	2.44	ribophorin; Rpn	D31717
98081_at	0.00	0.00	0.00	2.75	3.10	2.31	RPO1-3	AI853173
113001_at	0.00	0.00	0.00	2.04	1.65	0.00	RPS12	AI643492
101922_at	0.00	1.67	1.76	4.37	4.88	4.01	RPS8	AW123408
100612_at	0.00	0.00	2.89	0.00	0.00	0.00	ribonucleotide reductase M1; Rrm1	K02927
102001_at	0.00	4.09	4.93	4.37	4.89	2.47	ribonucleotide reductase M2; Rrm2	M14223
101584_at	0.00	0.00	0.00	0.00	2.07	2.03	Ras suppressor protein 1; Rsu1	X63039
92399_at	1.56	5.32	7.63	16.64	13.11	6.52	transcription factor 1; Runx1	D26532
92676_at	0.00	1.60	2.51	4.67	13.58	14.15	transcription factor 2; Runx2	D14636
92539_at	0.00	2.45	2.84	3.90	5.12	4.18	protein A11 (calgizzarin); S100a10	M16465
98600_at	1.80	2.47	2.93	4.55	7.43	6.03	binding protein A11; S100a11	U41341
100959_at	0.00	1.56	0.00	2.63	2.65	2.69	binding protein A13; S100a13	X99921
100960_g_at	0.00	0.00	0.00	1.80	2.42	2.42	binding protein A13; S100a13	X99921
92770_at	0.00	0.00	1.83	2.72	2.37	2.61	protein A6 (calcyclin); S100a6	X66449
95754_at	0.00	0.00	0.00	0.00	2.08	2.47	UNK_AI838216	AI838216
102712_at	-3.84	2.96	4.98	8.61	4.23	0.00	Saa3	X03505
102012_at	0.00	3.45	2.78	6.04	4.14	5.35	SAPS	AB014485
97340_at	0.00	0.00	0.00	0.00	9.89	4.81	SART3	AI839599
96657_at	0.00	0.00	2.35	3.95	3.54	3.47	N1-acetyl transferase; Sat	L10244
99127_at	0.00	0.00	0.00	2.14	2.18	2.16	ataxia 10 homolog (human); Sca10	X61506
95758_at	0.00	0.00	1.71	3.17	5.87	3.76	A desaturase 2; Scd2	M26270
103244_at	0.00	2.16	1.90	6.42	14.12	8.60	SCGF	AB009245
101132_at	0.00	0.00	0.00	0.00	2.13	0.00	voltage-gated, type VI, alpha polypeptide; Scn6a	L36179
92755_f_at	0.00	0.00	0.00	3.02	0.00	0.00	secretin; Sct	X73580
94140_at	0.48	2.44	-2.79	0.00	0.00	0.00	SCVR	M59446

93717_at	2.82	3.56	-0.43	1.69	2.72	-0.33	cytokine A12; Scya12	U50712
102736_at	2.71	5.21	6.15	9.01	7.67	2.10	small inducible cytokine A2; Scya2	M19681
92849_at	2.26	2.31	0.00	0.00	0.00	0.00	small inducible cytokine A6; Scya6	M58004
94761_at	3.20	6.30	7.57	6.75	7.08	0.00	SCYA7	X70058
104388_at	2.37	2.97	2.84	3.61	2.34	5.38	SCYA9	U49513
93858_at	0.00	0.00	4.64	3.50	1.42	1.46	cytokine B subfamily (Cys-X-Cys), member 10; Scyb10	M33266
96953_at	0.00	3.54	0.00	2.92	2.95	0.00	KEC	AW120786
98772_at	3.38	5.10	0.00	2.26	0.00	0.00	cytokine B subfamily, member 5; Scyb5	U27267
98008_at	0.00	0.00	0.00	0.00	5.32	0.00	cytokine subfamily D, 1; Scyd1	U92565
96033_at	0.00	0.00	0.00	0.00	3.39	3.96	syndecan 1; Sdc1	Z22532
95104_at	0.00	0.00	0.00	0.00	7.78	5.08	syndecan 2; Sdc2	U00674
98590_at	0.00	1.50	0.00	0.00	5.17	2.08	syndecan 4; Sdc4	D89571
93017_at	0.00	2.05	2.50	2.98	2.03	2.97	SDCBP	AF077527
110314_at	0.00	0.00	0.00	3.88	0.00	0.00	UNK_AA939505	AA939505
93503_at	3.23	2.68	3.83	5.83	5.65	6.03	SDF5	U88567
103421_at	0.00	0.00	0.00	2.75	2.23	4.03	factor receptor 2; Sdfr2	D50464
102319_at	0.00	0.00	0.00	0.00	2.38	0.00	SDP8	AF062484
110816_at	0.00	1.86	2.60	3.96	4.31	4.31	SEC22L1	AI836222
103953_at	0.00	0.00	0.00	4.26	4.62	2.88	trafficking protein-like 1 (S. cerevisiae); Sec22l1	U91538
93711_at	0.00	0.00	0.00	0.00	2.09	0.00	SEC23A (S. cerevisiae); Sec23a	D12713
98944_at	0.00	2.50	3.56	6.12	3.76	3.03	UNK_AI848343	AI848343
97882_at	0.00	2.61	2.86	6.48	9.11	5.92	SEC61A	AB032902
92870_at	0.00	0.00	0.00	2.77	0.00	0.00	SEL1H	AF063095
100457_at	0.00	0.00	0.00	2.17	2.21	2.29	selectin, endothelial cell, ligand; Selel	X84037
104692_at	0.00	2.30	0.00	0.00	0.00	0.00	SELP	M72332
94063_at	0.00	0.00	0.00	0.00	4.29	0.00	[illegible] immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A;	X85991
103094_at	0.00	0.00	0.00	0.00	5.61	4.54	SERF1	AI036894
102641_at	0.00	7.13	3.23	5.34	3.39	11.03	SFPI1	L03215
97997_at	0.00	4.24	6.40	9.69	9.18	2.33	secreted frizzled-related sequence protein 1; Sfrp1	U88566
104672_at	0.00	0.00	0.00	0.00	12.10	0.00	secreted frizzled-related sequence protein 3; Sfrp3	U68058
95791_s_at	0.00	0.00	0.00	2.66	2.33	0.00	[illegible] arginine/serine-rich 10,splicing factor, arginine/serine-rich 2 (SC-35); Sfrs10,Sfrs2	U14648
94017_s_at	0.00	0.00	0.00	2.08	0.00	0.00	SFRS2	X98511

101004_f_at	0.00	2.16	2.00	2.68	2.36	2.18	splicing factor, arginine/serine-rich 3 (SRp20); Sfrs3	X91656
101861_at	0.00	0.00	0.00	0.00	2.24	2.47	SGCE	AF031919
96127_at	0.00	2.31	2.89	3.47	3.36	6.40	SGPL1	AW048730
93806_at	0.00	2.17	2.28	2.89	3.44	5.41	UNK_AI848671	AI848671
92975_at	0.00	2.44	2.15	2.25	2.45	3.07	SH3-domain binding protein 2; Sh3bp2	L14543
103755_at	0.00	0.00	0.00	2.54	5.91	3.28	SH3 domain protein D19; Sh3d19	D89677
93275_at	0.00	0.50	0.00	2.58	5.00	4.00	SH3 domain protein 2B; Sh3d2b	U58885
99158_at	0.00	1.76	1.70	3.10	2.59	2.16	SH3 domain protein 3; Sh3d3	U58888
95456_r_at	0.00	0.00	0.00	0.00	2.03	1.83	deleted gene 1; Shfdg1	U41626
99042_s_at	0.00	0.00	0.00	2.57	4.04	6.81	SHOX2	U66918
102752_at	0.00	2.08	2.08	3.26	1.98	2.62	SHYC	AF072697
94432_at	0.00	0.00	0.00	0.00	2.68	3.64	UNK_AI117157	AI117157
99847_at	0.00	0.00	0.00	0.00	3.29	3.93	Siat4	X73523
95599_at	0.00	0.00	0.00	0.00	4.82	3.35	sialyltransferase 4c; Siat4c	D28941
94492_at	0.00	0.00	0.00	2.96	3.59	4.98	UNK_AB025406	AB025406
99655_at	0.00	0.00	0.00	2.64	2.61	2.30	UNK_AB025405	AB025405
95144_at	0.00	0.00	0.00	2.28	1.75	1.94	UNK_AB024984	AB024984
97489_at	0.00	0.00	0.00	0.00	2.58	3.90	UNK_AI846739	AI846739
93789_s_at	0.00	1.63	0.00	2.55	3.08	3.28	SIN3B	AF038848
92450_at	0.00	0.00	0.00	0.00	2.37	2.54	SLC12A4	AF047339
104719_at	0.00	2.21	0.00	0.00	3.05	2.14	SLC12A7	AI182203
100491_at	0.00	0.00	0.00	1.90	2.76	0.00	SLC16A2	AF045692
100943_at	0.00	0.00	0.00	7.00	7.27	2.37	neutral amino acid transporter; Slc1a4	U75215
103065_at	0.00	1.93	0.00	4.69	6.26	3.25	20, member 1; Slc20a1	M73696
99112_at	0.00	0.00	0.00	0.00	1.63	3.71	SLC25A10	AA683883
97473_at	0.00	8.03	4.82	19.23	14.32	7.15	SLC25A17	AW124470
97472_at	0.00	0.00	0.00	2.35	2.52	0.00	SLC25A17	AJ006341
100618_f_at	0.00	0.00	0.00	5.23	4.78	7.59	25 (mitochondrial carrier; adenine nucleotide translocator), member 5; Slc25a5	AA062013
97957_at	0.00	0.00	0.00	0.00	2.19	0.00	SLC27A4	AF072759
95733_at	0.00	0.00	0.00	0.00	3.22	3.31	UNK_AI838274	AI838274
95571_at	0.00	0.00	0.00	0.00	1.83	2.40	SLC30A4	AF004100
101877_at	0.00	1.78	1.74	2.74	3.70	3.40	SLC31A1	AI854432
103845_at	0.00	0.00	0.00	2.78	2.72	0.00	UNK_AI839005	AI839005
93558_at	0.00	0.00	0.00	2.33	3.66	2.36	SLC35A2	AB027147
100020_at	0.00	0.00	0.00	0.00	3.18	6.84	solute carrier family 4 (anion exchanger), member 2; Slc4a2	J04036
103818_at	0.00	3.94	0.00	0.00	7.66	4.45	SLC7A7	AJ012754
104214_at	0.00	2.48	0.00	0.00	0.00	0.00	SLC7A8	AW122706
99524_at	0.00	0.00	0.00	2.03	0.00	0.00	solute carrier family 8 (sodium/calcium exchanger), member 1; Slc8a1	AF004666
102264_at	2.09	0.00	2.47	2.09	1.99	2.48	SLFN1	AF099972
92472_f_at	2.33	3.93	4.37	4.87	3.05	3.83	SLFN2	AF099973

92471_i_at	0.00	3.71	3.39	5.90	8.39	4.15	SLFN2	AF099973
92858_at	0.00	4.23	2.55	6.22	7.43	3.89	SLPI	AF002719
99552_at	3.78	17.54	20.88	10.28	11.85	25.49	slug, chicken homolog; Slugh	U79550
96050_at	0.00	0.00	0.00	7.04	4.66	0.00	SMARCB1	AJ011740
102062_at	0.00	0.00	4.08	0.00	4.73	3.19	matrix associated, actin dependent regulator of chromatin, subfamily c, member 1;	U85614
106277_at	0.00	0.00	0.00	2.18	2.30	3.29	UNK_AW120530	AW120530
96812_at	0.00	0.00	0.00	2.57	6.03	2.71	SMOH	AF089721
103830_at	0.00	2.85	0.00	0.00	3.62	1.44	snail homolog, (Drosophila); Sna	M95604
101530_at	0.00	0.00	0.00	2.32	2.60	1.69	ribonucleoprotein 116 kDa; Snrp116-pending	U97079
101506_at	0.00	0.00	0.00	2.55	0.00	0.00	UNK_AW227345	AW227345
100577_at	0.00	0.00	2.41	0.00	2.31	2.11	small nuclear ribonucleoprotein D1; Snrpd1	M58558
112282_s_at	0.00	3.18	4.02	4.54	4.18	4.52	UNK_AI154073	AI154073
112283_at	1.68	2.68	0.00	3.14	7.08	5.94	UNK_AA718584	AA718584
94550_at	0.00	2.19	1.41	1.85	1.56	2.92	UNK_AW121324	AW121324
94902_at	0.00	1.87	0.00	2.17	2.23	1.87	dismutase 3, extracellular; Sod3	U38261
111853_at	0.00	0.00	0.00	1.50	4.58	3.78	SOUL-PENDING	AA726177
104408_s_at	0.00	0.00	0.00	0.00	2.29	2.61	SRY-box containing gene 18; Sox18	L35032
101430_at	0.00	0.00	0.00	2.09	4.36	6.01	SOX4	AW124153
100032_at	0.00	0.00	0.00	2.03	2.18	0.00	transcription factor 1; Sp1	X60136
113152_at	0.00	0.00	0.00	1.99	2.66	0.00	SPAK-PENDING	AI850672
97160_at	0.00	0.00	0.00	3.53	3.24	3.71	cysteine rich glycoprotein; Sparc	X04017
97817_at	0.00	1.94	1.93	3.63	3.06	3.46	UNK_AW121136	AW121136
104374_at	0.00	5.69	5.43	8.11	4.63	0.00	serine protease inhibitor 2-2; Spi2-2	M64086
96060_at	0.00	0.00	0.00	2.21	1.73	1.92	serine protease inhibitor 3; Spi3	U25844
97487_at	0.00	0.00	0.00	0.00	2.61	6.46	serine protease inhibitor 4; Spi4	X70296
98405_at	0.00	0.00	0.00	0.00	5.15	0.00	serine protease inhibitor 6; Spi6	U96700
102125_f_at	0.00	0.00	1.30	0.00	2.11	0.00	SPI6	AI838923
99528_at	0.00	0.00	0.00	0.00	1.58	2.19	SPIN	AW122015
99563_at	0.00	0.00	0.00	0.00	1.95	2.49	SPIN	AW124681
97519_at	2.00	2.60	5.99	14.15	24.33	29.32	SPP1	X13986
94322_at	0.00	2.38	2.44	0.00	3.97	0.56	squalene epoxidase; Sqle	D42048
100095_at	0.00	0.00	0.00	1.76	1.71	2.24	scavenger receptor class B1; Srb1	U37799
96712_at	0.00	0.00	0.00	5.45	0.00	0.00	UNK_AI848508	AI848508
92540_f_at	0.00	2.10	2.30	7.95	5.95	3.58	SRM	Z67748
103568_at	0.00	2.43	4.42	4.07	17.64	6.56	SRPX-PENDING	AB028049
92265_f_at	0.00	0.00	0.00	0.00	1.91	3.63	SSA2	AF042139
99610_at	0.00	0.00	0.00	0.00	1.96	2.34	synovial sarcoma, translocated to X chromosome; Ssxt	X93357

101465_at	0.00	0.00	0.00	3.32	2.28	4.66	signal transducer and activator of transcription 1; Stat1	U06924
115806_at	0.00	0.00	3.13	2.81	0.00	0.00	UNK_AI851966	AI851966
99100_at	0.00	0.00	0.00	0.00	2.73	0.00	STAT3	AI837104
94331_at	0.00	2.04	0.00	0.00	2.15	2.15	signal transducer and activator of transcription 6; Stat6	L47650
93272_at	0.00	0.00	0.00	0.00	2.30	2.62	STK16	AF062076
98996_at	0.00	2.59	2.69	3.64	4.59	2.59	STK18	L29480
92639_at	0.00	1.93	0.00	2.47	2.35	0.00	serine/threonine kinase 6; Stk6	U80932
96076_at	0.00	0.00	0.00	2.18	3.12	2.49	UNK_AW121716	AW121716
99146_at	0.00	0.00	0.00	1.89	3.17	3.15	UNK_AW124355	AW124355
97983_s_at	0.00	0.00	0.00	0.00	2.13	0.00	syntaxin binding protein 1; Stxbp1	D45903
95703_at	0.00	0.00	0.00	3.28	1.98	1.70	UNK_AB024303	AB024303
101901_at	0.00	0.00	2.31	2.55	1.48	1.72	SUPL15H	AB024713
96542_at	0.00	0.00	0.00	0.00	4.43	4.05	surfeit gene 4; Surf4	M62606
97238_at	0.00	1.75	2.05	1.79	1.87	0.00	TACC3	AW209238
93541_at	0.00	0.00	0.00	2.16	3.73	0.00	TAGLN	Z68618
93333_at	0.00	0.00	2.00	2.33	2.00	2.02	Tbca	U05333
98937_at	0.00	0.00	1.55	3.06	3.36	2.94	TBRG1	AW049795
104655_at	0.00	0.00	0.00	0.00	1.42	2.13	UNK_AA755817	AA755817
97994_at	0.00	0.00	0.00	0.00	8.61	7.06	TCF7	AI019193
97995_at	0.00	0.00	0.00	0.00	2.94	2.18	7, T-cell specific; Tcf7	X61385
97901_at	0.00	0.00	0.00	0.00	3.66	0.00	transcription factor UBF; Tcfubf	X60831
93736_at	0.00	0.00	0.00	0.00	1.97	3.23	TCN2	AF090686
101540_at	0.00	0.00	0.00	1.89	2.12	1.40	TDG	AF069519
108581_at	0.00	0.00	0.00	0.00	2.46	4.50	UNK_AI835817	AI835817
116324_g_at	0.00	0.00	0.00	0.00	1.48	2.45	TEDP2-PENDING	AI851893
93367_at	0.00	0.00	0.00	2.20	3.14	3.08	associated protein 1; Tep1	U86137
103385_at	0.00	0.00	0.00	1.97	2.16	1.87	teratocarcinoma expressed, serine rich; Tera	U64033
99138_at	0.00	2.50	0.00	2.37	2.41	2.06	TFG	AA756292
98514_at	0.00	0.00	0.00	3.17	4.49	2.87	TFPI	AF004833
94383_at	0.00	0.00	0.00	4.72	5.97	5.52	pathway inhibitor 2; Tfpi2	D50586
101918_at	0.00	0.00	0.00	0.00	11.46	8.03	TGFB1	AJ009862
98019_at	0.00	0.00	0.00	0.00	8.41	3.84	factor beta 1 induced transcript 1; Tgfb1i1	L22482
93728_at	0.00	2.12	2.20	3.09	3.15	2.65	factor beta 1 induced transcript 4; Tgfb1i4	X62940
93300_at	0.00	0.00	0.00	0.00	3.26	0.00	transforming growth factor, beta 2; Tgfb2	X57413
102751_at	0.00	0.00	0.00	3.15	3.21	1.80	transforming growth factor, beta 3; Tgfb3	M32745
92877_at	2.66	4.57	4.66	7.44	3.85	2.47	transforming growth factor, beta induced, 68 kDa; Tgfbi	L19932
101502_at	0.00	0.00	2.62	4.72	4.01	3.84	TG interacting factor; Tgif	X89749
104601_at	0.00	2.79	0.00	0.00	2.21	0.00	Thbd	X14432

94930_at	0.00	0.00	0.00	6.81	11.52	6.37	Thbs2	L07803
103869_at	0.00	0.00	4.33	17.37	14.36	8.82	protein,mucin 1, transmembrane,thrombospondin 3; LOC54129,Muc1,Thbs3	U16175
99057_at	0.00	1.45	0.00	2.57	3.87	1.98	THY1	M12379
93071_at	0.00	0.00	0.00	2.37	2.57	1.98	TIF1B	X99644
93507_at	0.00	0.00	0.00	0.00	3.00	3.30	tissue inhibitor of metalloproteinase 2; Timp2	X62622
103671_at	0.00	0.00	0.00	0.00	3.68	2.01	TIP30-PENDING	AF061972
102273_at	0.00	0.00	0.00	1.73	2.46	1.93	TJ6	M31226
99935_at	0.00	0.00	0.00	0.00	2.21	2.70	tight junction protein 1; Tjp1	D14340
96081_at	0.00	0.00	0.67	0.00	8.09	0.00	TK1	X60980
110423_at	0.00	0.00	0.00	0.00	6.50	2.22	UNK_AA895554	AA895554
104623_at	0.00	0.00	0.00	0.00	2.35	3.25	enhancer of split 3, homolog of Drosophila E(spl);	X73360
98304_at	0.00	1.55	0.00	2.11	1.46	1.57	TLR6	AB020808
92555_at	0.00	0.00	2.39	3.84	11.52	5.85	UNK_AF053454	AF053454
100039_at	0.00	0.00	0.00	2.65	5.36	3.33	UNK_AW125880	AW125880
115179_at	0.00	2.54	0.00	0.00	0.00	0.00	UNK_AA718842	AA718842
99013_f_at	0.00	1.67	0.00	2.36	3.05	3.11	TMOD3	AI846797
115913_at	0.00	0.00	0.00	2.69	4.01	3.29	TMOD3	AI526875
101993_at	0.00	3.87	7.79	16.34	19.51	19.59	tenascin C; Tnc	X56304
98474_r_at	0.00	1.62	2.24	1.98	1.85	2.10	factor induced protein 6; Tnfip6	U83903
102887_at	0.00	0.00	0.00	0.00	10.64	3.70	OPG	U94331
92793_at	0.00	3.30	0.00	2.34	3.22	2.94	TNFRSF1A	X57796
94928_at	0.00	1.58	2.10	2.39	1.72	3.94	TNFRSF1B	X87128
93416_at	0.00	1.93	1.50	0.00	2.12	4.02	factor (ligand) superfamily, member 11; Tnfsf11	AF019048
100593_at	0.00	0.00	0.00	0.00	12.73	3.78	TNNT2	L47600
99578_at	0.00	1.98	3.26	3.07	3.45	1.98	TOP2A	U01915
95505_at	0.00	0.00	0.00	2.60	0.00	0.00	TOR1B	AW060509
97557_at	0.00	0.00	0.00	0.00	3.90	0.00	TOR2A	AI841457
95345_at	0.00	0.00	0.00	1.80	3.25	2.14	TPBG	AJ012160
103032_at	0.00	0.00	0.00	0.00	2.37	2.26	TPST1	AF038008
94948_at	0.00	0.00	0.00	0.00	4.95	4.19	TRIP6	AF097511
104154_at	0.00	2.21	0.00	0.00	4.07	0.00	TRP53	AB021961
104275_g_at	0.00	0.00	0.00	0.00	2.73	0.00	TRP53	AB021961
96183_at	0.00	0.00	2.23	0.00	2.20	2.47	UNK_AW122985	AW122985
93538_at	0.00	0.00	0.00	2.02	0.00	0.00	TTRAP-PENDING	AW228036
100342_i_at	0.00	2.12	2.24	4.45	5.18	2.86	TUBA1	M28729
100343_f_at	0.00	1.98	2.03	3.13	2.91	2.34	TUBA1	M28729
98759_f_at	0.00	2.05	1.98	3.16	3.39	2.73	TUBA2	M28727
101543_f_at	0.00	2.06	2.24	3.40	3.14	2.65	TUBA6	M13441
94835_f_at	0.00	2.92	2.73	4.98	5.58	3.49	Tubb2	M28739
94788_f_at	0.00	3.11	3.62	5.63	6.28	4.29	Tubb5	X04663
94789_r_at	0.00	7.98	8.12	78.06	13.75	7.31	Tubb5	X04663
98028_at	0.00	0.00	1.73	1.28	5.13	7.55	TWIST	M63649
92807_at	0.00	1.60	2.05	2.73	2.29	2.42	TXN	X77585
93237_s_at	0.00	1.82	0.00	0.00	4.28	3.89	TYMS	AU044050
100397_at	2.04	3.39	3.70	5.63	5.00	12.41	TYROBP	AF024637
97304_at	0.00	0.00	0.00	0.00	2.07	2.44	UBP1	AI836100
98972_at	0.00	0.00	0.00	0.00	5.36	2.56	UNK_AI574262	AI574262

94197_at	0.00	3.03	0.00	2.40	3.38	0.00	UGCG	D89866
102322_at	2.51	2.38	2.67	3.94	4.24	4.11	UGDH	AF061017
95024_at	1.90	0.00	3.20	3.26	2.42	0.00	USP18	AW047653
93305_f_at	0.00	0.00	5.69	4.47	3.95	3.50	VAMP8	AF053724
100345_f_at	0.00	0.00	0.00	2.62	2.67	2.60	VAMP8	W65964
101982_at	0.00	1.36	0.00	2.45	2.66	2.27	stimulated phosphoprotein;	X98475
99799_at	1.44	3.13	0.00	2.64	2.99	2.40	vav oncogene; Vav	X64361
96511_s_at	0.00	0.00	0.00	0.00	2.07	0.00	vav oncogene; Vav	D83266
95490_at	0.00	0.00	0.00	2.26	3.00	2.09	UNK_AW120891	AW120891
92558_at	0.00	3.13	0.00	4.11	5.49	11.07	VCAM1	M84487
92559_at	1.22	1.55	0.00	0.00	2.01	2.67	VCAM1	U12884
92560_g_at	0.00	0.00	0.00	0.00	3.35	4.56	VCAM1	U12884
100084_at	0.00	0.00	0.00	0.00	2.73	3.56	villin 2; Vil2	X60671
101047_at	0.00	0.00	0.00	0.00	2.12	1.73	VIM	AW123697
93337_at	0.00	0.00	0.00	2.13	1.83	2.11	sorting 4b (yeast); Vps4b	U10119
98963_at	0.00	2.85	0.00	0.00	4.71	3.54	VRL1	AB021665
100522_s_at	0.00	0.00	0.00	3.20	3.75	3.21	WW domain binding protein 5; Wbp5	U92454
100523_r_at	0.00	0.00	0.00	2.41	3.13	2.02	WW domain binding protein 5; Wbp5	U92454
103690_at	0.00	3.29	2.41	5.12	3.55	5.88	UNK_AW125574	AW125574
96075_at	0.00	2.11	0.00	3.70	2.89	3.37	WDR1	AW060876
92262_at	0.00	0.00	0.00	0.00	3.19	0.00	WIG1	AF012923
102044_at	0.00	2.42	3.42	11.06	23.81	19.33	ELM1	AF100777
102891_at	0.00	0.00	0.00	1.63	2.46	2.59	WRN	D86527
113110_at	0.00	0.00	0.00	0.00	2.42	3.11	WRN	AA960405
98946_at	0.00	1.87	0.00	4.72	3.95	3.55	UNK_AF033186	AF033186
113094_at	0.00	0.00	0.00	0.00	3.83	0.00	UNK_AA175692	AA175692
100958_at	0.00	0.00	0.00	0.00	4.56	7.64	UNK_AI647003	AI647003
99126_at	0.00	0.00	0.00	0.00	2.03	3.61	inactive X specific transcripts; Xist	L04961
92665_f_at	0.00	0.00	0.00	0.00	1.94	2.01	regulated complex; Xlr	X07967
100015_at	0.00	0.00	0.00	0.00	2.30	0.00	viral (v-yes) oncogene homolog; Yes	X67677
104400_at	0.00	2.18	0.00	2.06	3.18	2.96	UNK_AF076956	AF076956
97229_at	0.00	0.00	0.00	2.05	0.00	0.00	UNK_AW061042	AW061042
97535_at	0.00	1.63	2.14	2.89	2.41	2.21	monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide;	D87661
97061_g_at	0.00	1.94	2.17	2.75	3.19	3.36	YWHAQ	AW215489
97544_at	0.00	1.72	0.00	2.31	3.14	2.92	YWHAZ	D83037
92501_s_at	0.00	0.00	0.00	0.00	5.24	4.39	ZAC1	X95503
92502_at	0.00	0.00	0.00	1.40	7.40	6.62	ZAC1	X95504
100475_at	0.00	0.00	0.00	3.36	2.20	2.88	zinc finger protein 147; Zfp147	D63902
92771_at	0.00	0.00	0.00	0.00	2.13	1.97	ZFP207	AB013357
102277_at	0.00	0.00	0.00	0.00	2.59	0.00	ZFP26	M36514
92934_at	0.00	0.00	0.00	0.00	2.66	0.00	zinc finger protein 90; Zfp90	X79828
103676_at	0.00	0.00	0.00	0.00	2.06	2.03	UNK_AI551306	AI551306

Table 2								
Treatment	BMP2	BMP2	BMP2	BMP2	BMP2	BMP2		
Time	day 01	day 02	day 03	day 04	day 07	day 14		
Affymetrix Qualifier	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Avg. Fold Change	Gene Name	Genbank Accession #
115844_at	-2.74	-4.65	-3.15	-2.76	-2.12	-2.10	UNK_AI847028	AI847028
103494_at	0.00	-2.50	-3.42	-2.87	-4.24	-2.99	UNK_AI047972	AI047972
104342_i_at	0.00	-4.22	-3.45	-5.08	-10.18	-4.00	UNK_AI845798	AI845798
107074_at	0.00	-2.55	-2.53	-3.42	-4.39	-2.24	UNK_AI838083	AI838083
133738_at	0.00	-2.30	-2.02	-3.17	-4.39	-3.23	UNK_AI467229	AI467229
133932_at	0.00	-2.17	-2.06	-3.16	-4.05	-2.76	UNK_AI503993	AI503993
133951_at	0.00	-3.22	-3.10	-10.36	-6.86	-2.39	UNK_AI504979	AI504979
94534_at	0.00	-2.04	-2.11	0.00	-4.07	-2.36	UNK_AI835446	AI835446
94790_at	0.00	-2.24	-2.48	0.00	-3.80	-2.57	UNK_AA681807	AA681807
95468_at	0.00	-2.15	-1.91	-2.63	-4.12	-2.55	BTD	AI850202
96391_at	0.00	-2.96	-2.60	-1.90	-3.00	-2.41	EST; unknown	C80836
105638_at	0.00	-3.95	-4.59	0.00	-10.36	-2.07	UNK_AA896641	AA896641
106963_at	0.00	-2.48	-2.10	0.00	-3.26	-3.68	UNK_AW050323	AW050323
107282_at	0.00	-2.07	-2.27	0.00	-4.69	-4.22	UNK_AW047933	AW047933
107418_at	0.00	-2.16	0.00	-3.07	-5.71	-2.08	UNK_AW046245	AW046245
107952_i_at	0.00	-2.62	-2.43	0.00	-2.93	-2.12	UNK_AA606601	AA606601
109968_at	0.00	-5.91	-3.57	0.00	-8.76	-2.67	UNK_AA771415	AA771415
110269_at	-2.16	-5.45	-2.93	0.00	-3.03	0.00	UNK_AW045975	AW045975
115109_at	0.00	-2.05	-1.79	-4.17	-4.31	-2.28	UNK_AI838503	AI838503
115246_at	0.00	-1.95	-2.61	-3.31	-5.64	-2.62	UNK_AA790442	AA790442
116614_at	0.00	-2.54	-2.37	0.00	-3.72	-2.01	UNK_AA647405	AA647405
129661_at	0.00	-2.57	-3.45	0.00	-3.41	-2.12	UNK_AA792999	AA792999
130718_at	0.00	-2.98	-2.27	0.00	-2.50	-2.32	UNK_AI844247	AI844247
133977_at	0.00	-3.33	-2.14	-3.11	-2.79	-1.68	UNK_AI506633	AI506633
135609_at	0.00	-2.66	0.00	-2.42	-4.25	-2.42	UNK_AI505553	AI505553
93514_at	0.00	-2.76	-1.94	0.00	-4.77	-5.23	MYLC	X12972
94418_at	0.00	-2.71	-8.42	0.00	-2.51	-0.63	UNK_AI839004	AI839004
94908_r_at	0.00	0.00	-2.19	0.00	-4.76	-2.57	UNK_AW045632	AW045632
95587_at	0.00	-2.33	-2.23	0.00	-2.97	-1.80	UNK_AI837204	AI837204
98942_r_at	0.00	-2.33	-3.05	0.00	-3.93	-1.78	UNK_AW125284	AW125284
102862_at	0.00	0.00	-3.42	0.00	-3.42	-3.17	UNK_AA873956	AA873956
102916_s_at	0.00	-4.25	-3.83	0.00	-2.86	0.00	UNK_AB010266	AB010266
102922_at	0.00	-3.08	-2.52	0.00	-2.84	-1.50	UNK_AI851387	AI851387
105610_at	0.00	0.00	-2.89	0.00	-4.34	-2.22	UNK_AA388982	AA388982
106934_at	0.00	0.00	-2.79	0.00	-10.65	-4.94	UNK_AW047806	AW047806
107569_at	0.00	-2.01	0.00	0.00	-2.37	-2.03	UNK_AA738625	AA738625
110774_at	0.00	-3.03	-2.48	0.00	-2.45	-1.51	UNK_AI852667	AI852667
111228_at	0.00	-1.68	-2.69	0.00	-2.72	-2.01	UNK_AW122874	AW122874
111254_at	0.00	-2.06	-2.12	0.00	-3.40	-1.69	UNK_AA735016	AA735016
111260_at	0.00	0.00	-2.66	0.00	-3.27	-3.11	UNK_AI843809	AI843809
112012_at	0.00	-2.13	-2.12	0.00	-4.16	-1.67	UNK_AI875092	AI875092
113124_at	0.00	-4.08	0.00	0.00	-8.64	-2.40	UNK_AI852911	AI852911
113806_at	0.00	0.00	-2.69	0.00	-2.68	-2.20	UNK_AW121611	AW121611
114138_at	0.00	0.00	-2.00	0.00	-5.82	-2.95	UNK_AI643851	AI643851
114297_f_at	0.00	-1.96	-2.03	0.00	-4.33	-2.31	UNK_AI021087	AI021087
114466_at	0.00	-1.89	-2.07	0.00	-3.21	-2.18	UNK_AA197511	AA197511
116583_at	0.00	-2.08	-1.70	0.00	-3.36	-2.23	UNK_AW121389	AW121389
116792_at	0.00	-1.94	-3.96	0.00	-4.51	-3.31	UNK_AI480742	AI480742
129309_at	0.00	-2.55	-1.92	0.00	-3.86	-2.58	UNK_AI596885	AI596885
129952_at	0.00	0.00	-2.17	0.00	-2.85	-2.68	UNK_AI595378	AI595378
135181_f_at	0.00	-1.74	-1.70	-2.21	-3.48	-2.24	UNK_AW125817	AW125817
139035_at	0.00	-2.05	0.00	-2.09	-2.40	0.00	UNK_AI846518	AI846518
140572_at	0.00	-2.94	-2.45	0.00	-2.88	0.00	UNK_AW125201	AW125201

92202_g_at	0.00	0.00	0.00	0.00	-3.21	-2.40	UNK_AI553024	AI553024
92941_at	0.00	0.00	0.00	0.00	-3.70	-2.71	UNK_AA833509	AA833509
93177_at	0.00	0.00	0.00	0.00	-3.03	-2.08	UNK_AW121661	AW121661
93780_at	0.00	-2.35	-1.92	0.00	-2.37	-1.95	UNK_AW060827	AW060827
95376_at	0.00	0.00	0.00	0.00	-5.44	-5.10	UNK_AJ011107	AJ011107
95518_at	0.00	-2.12	-1.76	0.00	-2.06	0.00	UNK_AW122893	AW122893
96211_at	0.00	0.00	0.00	-2.61	-4.19	0.00	UNK_AI846896	AI846896
99331_at	0.00	0.00	0.00	0.00	-3.02	-4.46	UNK_AW125581	AW125581
99503_at	0.00	-2.49	0.00	0.00	-2.85	-1.74	UNK_AW045204	AW045204
100058_at	0.00	0.00	0.00	0.00	-2.34	-3.75	UNK_AW047776	AW047776
103257_at	0.00	0.00	-1.75	0.00	-2.96	-2.37	UNK_AA690483	AA690483
103665_at	0.00	-2.26	-5.60	0.00	-1.79	-0.73	UNK_AW122523	AW122523
104153_at	0.00	0.00	0.00	0.00	-3.18	-2.04	UNK_AW047743	AW047743
104293_at	0.00	0.00	-1.95	0.00	-2.61	-2.73	UNK_AI882440	AI882440
104445_at	-1.69	-3.53	-2.56	0.00	-1.65	0.00	UNK_AW046694	AW046694
104491_at	0.00	-1.77	-2.21	0.00	-2.08	0.00	UNK_AI509330	AI509330
104804_at	0.00	-1.61	0.00	0.00	-2.94	-2.31	UNK_AI504570	AI504570
104944_at	0.00	0.00	0.00	0.00	-2.25	-2.14	UNK_AA619815	AA619815
105168_at	0.00	-1.76	0.00	0.00	-2.67	-2.61	UNK_AI847519	AI847519
105569_at	0.00	0.00	-1.98	0.00	-3.12	-3.32	UNK_AI605044	AI605044
105619_at	0.00	0.00	0.00	0.00	-20.58	-7.69	UNK_AI849242	AI849242
105706_at	0.00	0.00	0.00	0.00	-3.77	-2.26	UNK_AI847342	AI847342
106065_at	0.00	-2.29	0.00	0.00	-2.40	0.00	UNK_AI849096	AI849096
106297_at	0.00	-2.02	0.00	0.00	-2.32	0.00	UNK_AI841521	AI841521
106439_at	0.00	0.00	0.00	0.00	-3.25	-3.88	UNK_AI851838	AI851838
106505_at	0.00	-1.79	0.00	0.00	-2.85	-2.52	UNK_AI844271	AI844271
106521_at	0.00	-2.23	0.00	0.00	-4.38	0.00	UNK_AI987764	AI987764
106896_at	0.00	0.00	0.00	0.00	-2.96	-2.16	UNK_AW049892	AW049892
107400_at	0.00	-2.00	-2.22	0.00	-1.83	0.00	UNK_AW048204	AW048204
107427_at	0.00	-1.59	0.00	0.00	-3.02	-2.22	UNK_AW122504	AW122504
107428_at	0.00	0.00	0.00	0.00	-2.66	-2.13	UNK_AW046414	AW046414
108010_at	0.00	0.00	0.00	0.00	-3.82	-2.72	UNK_AW210455	AW210455
108069_at	0.00	0.00	0.00	0.00	-2.51	-2.13	UNK_AI642606	AI642606
108488_at	0.00	0.00	0.00	0.00	-2.80	-2.49	UNK_AI838112	AI838112
108565_at	0.00	-2.68	-2.95	0.00	2.66	4.55	UNK_AI853095	AI853095
108767_at	0.00	-2.42	0.00	0.00	-3.47	0.00	UNK_AI448797	AI448797
108822_at	0.00	0.00	0.00	-3.70	-3.72	0.00	UNK_AI615758	AI615758
109049_at	0.00	0.00	0.00	0.00	-3.89	-2.60	UNK_AI643675	AI643675
109086_at	0.00	0.00	-1.83	0.00	-3.02	-2.24	UNK_AI463271	AI463271
109488_at	0.00	0.00	0.00	0.00	-3.72	-3.74	UNK_AW123076	AW123076
109774_at	0.00	-1.85	-1.71	0.00	-3.33	-2.06	PDK2	AI848783
110330_at	0.00	-1.52	0.00	0.00	-4.15	-2.08	UNK_AI843917	AI843917
111483_at	0.00	-1.37	0.00	0.00	-4.16	-3.11	UNK_AI451767	AI451767
111525_at	0.00	0.00	0.00	0.00	-2.70	-2.28	UNK_AA289880	AA289880
111547_at	0.00	0.00	0.00	0.00	-3.17	-2.26	UNK_AI851666	AI851666
111970_at	0.00	-1.51	0.00	0.00	-4.74	-3.89	UNK_AI616223	AI616223
112392_at	0.00	0.00	0.00	0.00	-4.82	-2.89	UNK_AI834768	AI834768
112405_at	0.00	0.00	0.00	0.00	-5.07	-3.81	UNK_AI557974	AI557974
112864_at	0.00	-1.75	-2.07	0.00	-2.50	0.00	UNK_AI849524	AI849524
112986_at	0.00	0.00	0.00	0.00	-5.51	-5.79	UNK_AI849914	AI849914
113545_at	0.00	-1.47	0.00	0.00	-2.87	-2.16	UNK_AI847141	AI847141
113691_at	0.00	0.00	0.00	0.00	-3.69	-2.65	UNK_AW049533	AW049533
114315_at	0.00	0.00	0.00	0.00	-2.70	-2.60	UNK_AW048818	AW048818
114394_at	0.00	-2.13	0.00	0.00	-2.20	0.00	UNK_AW121080	AW121080
114420_at	0.00	-3.91	-3.29	0.00	3.25	4.37	UNK_AA734866	AA734866
114453_at	0.00	0.00	0.00	0.00	-4.76	-5.72	UNK_AI848077	AI848077
114514_at	0.00	0.00	0.00	-2.37	-2.33	-1.99	UNK_AI605635	AI605635
114553_at	0.00	0.00	0.00	0.00	-2.81	-2.15	UNK_AI414584	AI414584
114556_at	0.00	-1.81	-1.54	0.00	-2.17	-2.03	UNK_AI451747	AI451747

114685_at	0.00	-2.08	0.00	0.00	-2.83	0.00	UNK_AW123120	AW123120
114743_at	0.00	0.00	0.00	0.00	-4.86	-4.13	UNK_AI591553	AI591553
114775_at	0.00	0.00	0.00	0.00	-4.72	-2.22	UNK_AI005882	AI005882
115070_at	0.00	0.00	-1.91	0.00	-4.34	-2.05	UNK_AA711252	AA711252
115155_at	0.00	0.00	-1.72	0.00	-4.16	-3.45	UNK_AI853189	AI853189
115199_at	0.00	0.00	0.00	0.00	-3.57	-2.34	UNK_AA667270	AA667270
115201_at	0.00	0.00	0.00	0.00	-2.39	-2.04	UNK_AI851486	AI851486
115236_at	0.00	-2.07	0.00	0.00	-3.28	-1.93	UNK_AA824120	AA824120
115360_at	0.00	-1.81	0.00	0.00	-3.33	-2.68	UNK_AI839569	AI839569
115467_at	0.00	0.00	0.00	0.00	-2.94	-2.13	UNK_AI852809	AI852809
115539_at	0.00	-2.59	-1.92	0.00	-3.44	-1.93	UNK_AW045801	AW045801
115575_at	0.00	0.00	0.00	0.00	-2.04	-2.26	UNK_AI853953	AI853953
116042_at	0.00	0.00	-1.84	0.00	-3.19	-2.15	UNK_AI591726	AI591726
116350_at	0.00	0.00	0.00	0.00	-5.09	-3.88	UNK_AA981270	AA981270
116390_at	0.00	0.00	0.00	0.00	-3.43	-2.26	UNK_AI647836	AI647836
116644_at	0.00	0.00	-1.97	0.00	-2.74	-2.31	UNK_AI882312	AI882312
116747_at	0.00	-1.82	0.00	0.00	-3.27	-2.54	UNK_AI505458	AI505458
116826_at	0.00	-1.98	-2.47	0.00	-4.71	-1.89	UNK_AA616199	AA616199
117128_at	0.00	0.00	0.00	0.00	-2.27	-2.06	UNK_AI851602	AI851602
117208_at	0.00	-1.93	-1.88	0.00	-3.27	-2.57	UNK_AI838208	AI838208
117242_at	0.00	0.00	0.00	0.00	-5.22	-2.68	UNK_AI835553	AI835553
117280_at	0.00	0.00	0.00	0.00	-4.97	-5.55	UNK_AI835075	AI835075
128785_r_at	0.00	-2.02	0.00	0.00	-4.18	-1.97	UNK_AI049307	AI049307
128829_at	0.00	-1.71	0.00	-1.71	-2.81	-2.11	UNK_AA624027	AA624027
129503_at	0.00	-1.69	0.00	0.00	-3.59	-2.12	UNK_AI893884	AI893884
129544_at	0.00	0.00	0.00	0.00	-3.45	-2.71	UNK_AI156198	AI156198
130460_at	0.00	0.00	0.00	0.00	-2.29	-2.22	UNK_AI836434	AI836434
130990_at	0.00	0.00	0.00	0.00	-2.19	-2.38	UNK_AW047063	AW047063
131264_f_at	0.00	0.00	0.00	0.00	-2.03	-2.23	UNK_AA466676	AA466676
132021_at	0.00	0.00	0.00	0.00	-2.04	-2.33	UNK_AI429239	AI429239
132820_at	0.00	-2.10	0.00	-2.44	0.00	0.00	UNK_AI639670	AI639670
133719_f_at	0.00	0.00	0.00	0.00	-2.62	-2.46	UNK_AI463563	AI463563
133720_at	0.00	-1.88	0.00	0.00	-2.73	-3.37	UNK_AI464129	AI464129
133838_at	0.00	-1.90	0.00	-2.11	-2.82	0.00	UNK_AA420328	AA420328
134116_at	0.00	0.00	0.00	0.00	-2.70	-2.28	UNK_AI255188	AI255188
135201_at	0.00	-3.44	-2.08	0.00	2.29	3.08	UNK_AA420078	AA420078
136068_at	0.00	0.00	0.00	0.00	-2.93	-2.72	UNK_AI551047	AI551047
136348_at	0.00	0.00	-1.98	0.00	-3.82	-3.36	UNK_AW146057	AW146057
136535_at	0.00	0.00	-1.79	0.00	-2.03	-2.06	UNK_AI642422	AI642422
137185_i_at	0.00	0.00	0.00	0.00	-2.57	-2.24	UNK_AI840674	AI840674
138502_at	0.00	0.00	0.00	0.00	-2.66	-3.02	UNK_AI847438	AI847438
139022_at	0.00	0.00	-1.88	0.00	-3.62	-2.20	UNK_AI427762	AI427762
140015_at	0.00	0.00	0.00	0.00	-2.30	-2.18	UNK_AW215832	AW215832
92786_at	0.00	0.00	0.00	0.00	-2.31	0.00	UNK_AI626942	AI626942
92845_at	0.00	0.00	0.00	0.00	-2.11	0.00	UNK_AI843232	AI843232
93138_at	0.00	0.00	0.00	0.00	-2.26	0.00	UNK_AI853219	AI853219
93464_at	0.00	0.00	0.00	0.00	-2.24	0.00	UNK_AI561567	AI561567
93478_at	0.00	0.00	0.00	-1.69	-1.83	-2.11	UNK_AA612483	AA612483
93481_at	0.00	0.00	0.00	0.00	0.00	-2.06	UNK_AI846720	AI846720
93560_at	0.00	-1.90	0.00	0.00	-2.31	-1.66	UNK_AI845882	AI845882
93584_at	0.00	0.00	0.00	0.00	-2.69	-1.71	IGH-6	V00821
93815_at	0.00	0.00	0.00	0.00	-2.17	0.00	UNK_AI839425	AI839425
94010_g_at	0.00	0.00	0.00	0.00	-2.07	0.00	UNK_AI848888	AI848888
94057_g_at	-1.44	-2.04	0.00	0.00	-2.00	0.00	stearoyl-Coenzyme A desaturase 1; Scd1	M21285
94080_at	0.00	0.00	0.00	0.00	-2.49	0.00	UNK_AI835718	AI835718
94481_at	0.00	0.00	0.00	0.00	-2.14	-1.86	UNK_AI851321	AI851321

94531_at	0.00	0.00	0.00	0.00	-3.06	-1.99	UNK_AW124582	AW124582
94554_at	0.00	0.00	0.00	0.00	-2.75	0.00	UNK_AW120965	AW120965
94663_at	0.00	0.00	0.00	0.00	-2.21	0.00	0	AA407151
94806_at	0.00	0.00	0.00	0.00	-2.11	0.00	UNK_AW125336	AW125336
94807_at	0.00	0.00	-2.25	0.00	0.00	0.00	UNK_AI848354	AI848354
94870_f_at	0.00	0.00	0.00	0.00	-2.62	-1.84	UNK_AW124226	AW124226
94871_r_at	0.00	0.00	0.00	0.00	-4.12	0.00	UNK_AW124226	AW124226
94907_f_at	0.00	0.00	0.00	0.00	-2.76	-1.89	UNK_AW045632	AW045632
95026_at	0.00	0.00	0.00	0.00	-2.74	0.00	UNK_AW047688	AW047688
95031_at	0.00	0.00	0.00	0.00	-2.05	-1.89	UNK_AW060212	AW060212
95058_f_at	0.00	0.00	0.00	0.00	-2.18	0.00	UNK_AW121984	AW121984
95120_at	0.00	0.00	0.00	0.00	-2.27	0.00	UNK_AI837621	AI837621
95440_at	0.00	0.00	0.00	0.00	-2.82	0.00	UNK_AI846093	AI846093
95577_at	0.00	0.00	0.00	0.00	-2.67	-1.99	UNK_AW049625	AW049625
95905_at	0.00	0.00	0.00	0.00	0.00	-2.38	UNK_AI118078	AI118078
95952_at	0.00	-1.84	-1.82	-1.27	-2.86	-1.99	UNK_AW124781	AW124781
96095_i_at	0.00	0.00	0.00	0.00	-2.47	0.00	UNK_AI648018	AI648018
96096_f_at	0.00	0.00	0.00	0.00	-2.58	0.00	UNK_AI648018	AI648018
96122_at	0.00	-1.93	0.00	0.00	-2.80	0.00	UNK_AW049373	AW049373
96158_at	0.00	0.00	-1.77	0.00	-2.05	-1.69	UNK_AW123477	AW123477
96205_at	0.00	0.00	-1.84	0.00	-2.56	-1.72	SH3BGR	AW048272
96212_at	0.00	0.00	-1.93	0.00	-3.14	-1.65	UNK_AI853918	AI853918
96291_f_at	0.00	0.00	0.00	0.00	-2.41	-1.88	UNK_AI835847	AI835847
96572_at	0.00	0.00	0.00	0.00	-2.71	0.00	UNK_AW047232	AW047232
96634_at	0.00	0.00	0.00	0.00	-2.92	0.00	UNK_AI850090	AI850090
96670_at	0.00	0.00	0.00	0.00	-2.97	-1.69	UNK_AI841295	AI841295
96676_at	0.00	0.00	0.00	0.00	-2.01	0.00	UNK_AW121875	AW121875
96688_at	0.00	0.00	0.00	0.00	-2.29	0.00	UNK_AI845463	AI845463
96746_at	0.00	0.00	-1.92	0.00	-2.21	0.00	UNK_AW124813	AW124813
96747_at	0.00	0.00	0.00	0.00	-2.42	0.00	UNK_AW121294	AW121294
96756_at	0.00	0.00	0.00	0.00	-2.18	0.00	0	AA693236
96879_at	0.00	0.00	0.00	0.00	-2.07	0.00	UNK_AI852338	AI852338
96899_at	0.00	0.00	0.00	0.00	-2.32	0.00	UNK_AW123802	AW123802
96909_at	0.00	0.00	0.00	0.00	-2.23	0.00	UNK_AI849803	AI849803
96947_at	0.00	0.00	0.00	0.00	-2.18	0.00	UNK_AW046273	AW046273
97201_s_at	0.00	0.00	0.00	0.00	-2.03	0.00	UNK_AA823381	AA823381
97204_s_at	0.00	0.00	0.00	0.00	-2.02	0.00	UNK_AI850983	AI850983
97242_at	0.00	0.00	0.00	0.00	-2.05	-1.78	UNK_AI849011	AI849011
97447_at	0.00	0.00	0.00	0.00	-2.07	0.00	UNK_AI836718	AI836718
97773_at	0.00	0.00	-2.54	0.00	0.00	0.00	UNK_AI173145	AI173145
97869_at	0.00	0.00	-1.78	0.00	-2.27	0.00	UNK_AI844043	AI844043
98924_at	0.00	0.00	0.00	0.00	-3.31	-1.92	UNK_Y08027	Y08027
99159_at	0.00	0.00	0.00	0.00	-2.29	0.00	UNK_AI842675	AI842675
99441_at	0.00	0.00	0.00	0.00	-2.03	-1.79	UNK_AW123852	AW123852
99618_at	0.00	0.00	0.00	0.00	-2.07	0.00	UNK_AI853523	AI853523
99658_f_at	0.00	0.00	0.00	0.00	-2.32	0.00	UNK_AW047907	AW047907
99988_at	0.00	0.00	0.00	0.00	-2.14	-1.75	UNK_AW122115	AW122115
100042_at	0.00	0.00	-1.69	0.00	-2.14	0.00	UNK_AI837921	AI837921
100628_at	0.00	0.00	0.00	0.00	-2.01	0.00	UNK_AI840263	AI840263
100878_at	0.00	0.00	0.00	0.00	-2.22	0.00	UNK_AW124985	AW124985
100892_at	0.00	0.00	0.00	0.00	-2.38	0.00	UNK_AI850186	AI850186
101525_at	0.00	0.00	0.00	0.00	-2.24	0.00	UNK_AI848871	AI848871
101929_at	0.00	0.00	0.00	0.00	-2.09	-1.63	UNK_AI836322	AI836322
102000_f_at	0.00	0.00	0.00	0.00	-2.69	0.00	UNK_AI842835	AI842835
102022_at	0.00	0.00	-1.98	0.00	-2.33	0.00	UNK_AW124555	AW124555
102128_f_at	0.00	0.00	0.00	0.00	-2.27	0.00	UNK_C77227	C77227
102163_at	0.00	0.00	0.00	0.00	-4.48	0.00	UNK_X60388	X60388
102702_at	0.00	0.00	0.00	0.00	-2.14	-0.66	UNK_AI841487	AI841487
102845_at	0.00	0.00	0.00	0.00	-1.66	-2.14	UNK_AI836034	AI836034

103300_at	0.00	0.00	0.00	0.00	-2.06	0.00	UNK_AW124239	AW124239
103331_at	0.00	0.00	0.00	0.00	-1.61	-2.20	UNK_AI854450	AI854450
103484_at	0.00	0.00	0.00	0.00	-1.84	-2.16	UNK_AA619442	AA619442
103552_at	0.00	0.00	-2.03	0.00	0.00	0.00	UNK_AW046470	AW046470
103780_at	0.00	0.00	0.00	0.00	-2.47	0.00	UNK_AW049510	AW049510
103939_at	0.00	0.00	0.00	0.00	-2.16	0.00	UNK_AW121399	AW121399
103957_at	0.00	0.00	0.00	0.00	-2.38	2.04	transferrin receptor; Trfr	X57349
103998_at	0.00	-1.74	0.00	0.00	-2.23	0.00	UNK_AW122699	AW122699
103999_at	0.00	0.00	0.00	0.00	-1.59	-2.39	UNK_AI852034	AI852034
104034_at	0.00	0.00	0.00	0.00	-2.16	-1.70	UNK_AI846672	AI846672
104066_at	0.00	0.00	-1.97	0.00	0.00	-2.12	UNK_AI842192	AI842192
104212_at	0.00	0.00	0.00	0.00	-2.20	0.00	UNK_AA607767	AA607767
104229_at	0.00	0.00	0.00	0.00	-2.42	0.00	UNK_AI840035	AI840035
104258_at	0.00	0.00	0.00	0.00	-3.02	-1.84	UNK_AA881576	AA881576
104343_f_at	0.00	0.00	0.00	0.00	-2.20	-1.54	UNK_AI845798	AI845798
104356_at	0.00	0.00	0.00	0.00	0.00	-2.87	UNK_AI465543	AI465543
104745_at	0.00	0.00	0.00	0.00	-2.39	-1.80	UNK_AA763874	AA763874
104869_at	0.00	0.00	0.00	0.00	-3.21	0.00	UNK_AW049126	AW049126
104958_at	0.00	-1.85	0.00	0.00	-3.70	-1.99	UNK_AA170343	AA170343
105301_at	0.00	-1.94	0.00	0.00	-5.40	-1.39	UNK_AW121997	AW121997
105367_at	0.00	-1.91	0.00	0.00	-2.71	-1.86	UNK_AI605428	AI605428
105393_at	0.00	0.00	0.00	0.00	0.00	-3.00	UNK_AA416072	AA416072
105583_at	0.00	0.00	0.00	0.00	-3.25	-1.67	UNK_AI838647	AI838647
105635_at	0.00	0.00	0.00	0.00	-2.31	-1.66	UNK_AA920824	AA920824
105733_at	0.00	0.00	-1.87	0.00	-2.68	-1.62	UNK_AI844638	AI844638
105804_at	0.00	0.00	0.00	0.00	-2.78	0.00	UNK_AI847122	AI847122
105815_at	0.00	0.00	0.00	0.00	0.00	-2.97	UNK_AI851880	AI851880
106109_at	0.00	0.00	0.00	0.00	-2.98	0.00	UNK_AI843976	AI843976
106135_at	0.00	0.00	0.00	0.00	-2.34	-1.82	UNK_AI852401	AI852401
106225_at	0.00	0.00	0.00	0.00	-2.77	-1.69	UNK_AW048096	AW048096
106267_s_at	0.00	0.00	0.00	0.00	-2.06	-1.55	UNK_AW124033	AW124033
106268_at	0.00	-1.61	0.00	0.00	-2.23	-1.75	UNK_AI788609	AI788609
106573_at	0.00	-2.38	0.00	0.00	0.00	0.00	UNK_AW122342	AW122342
106600_at	0.00	0.00	0.00	0.00	-5.18	0.00	UNK_AW047323	AW047323
106815_at	0.00	0.00	0.00	-1.27	-2.07	0.00	UNK_AW047326	AW047326
106925_at	0.00	0.00	0.00	0.00	-2.61	-1.62	UNK_AW125887	AW125887
107001_at	0.00	0.00	-1.55	0.00	-3.54	-1.85	UNK_AW125170	AW125170
107002_at	0.00	0.00	0.00	0.00	-2.61	0.00	UNK_AI265696	AI265696
107085_at	0.00	0.00	0.00	0.00	-2.01	0.00	UNK_AW122784	AW122784
107099_at	0.00	0.00	-2.37	3.85	3.65	3.57	UNK_AA792731	AA792731
107139_at	0.00	0.00	0.00	0.00	-2.06	-1.58	UNK_AW123545	AW123545
107332_at	0.00	0.00	0.00	0.00	-3.03	-1.79	UNK_AW125461	AW125461
107534_at	0.00	0.00	0.00	0.00	-2.47	0.00	UNK_AI877261	AI877261
107545_at	0.00	-2.13	0.00	0.00	0.00	0.00	UNK_AI195408	AI195408
107555_at	0.00	0.00	0.00	0.00	-2.07	0.00	UNK_AW049421	AW049421
107626_at	0.00	0.00	0.00	0.00	-2.07	0.00	UNK_AA174516	AA174516
107817_at	0.00	-1.80	-1.98	0.00	-2.62	-1.77	UNK_AI481808	AI481808
107865_at	0.00	0.00	0.00	0.00	-2.55	-1.93	UNK_AW212116	AW212116
107953_r_at	0.00	0.00	0.00	0.00	-2.97	-1.99	UNK_AA606601	AA606601
107976_at	0.00	0.00	0.00	0.00	-2.37	-1.86	UNK_AI877204	AI877204
108032_at	0.00	-1.55	0.00	0.00	-2.52	-1.56	UNK_AI850652	AI850652
108084_at	0.00	-1.76	0.00	0.00	-2.45	-1.41	UNK_AA674925	AA674925
108095_at	0.00	-1.77	0.00	0.00	-2.32	-1.50	UNK_AW124440	AW124440
108357_at	0.00	0.00	0.00	0.00	0.00	-2.14	UNK_AA611398	AA611398
108493_at	0.00	-1.92	0.00	0.00	-2.21	-1.38	UNK_AI852390	AI852390
108537_at	0.00	-1.86	-1.87	0.00	-3.15	-1.61	UNK_AI846354	AI846354
108560_at	0.00	-1.66	0.00	0.00	-2.49	-1.49	UNK_AI849518	AI849518
108742_at	0.00	0.00	0.00	0.00	-2.00	-2.05	UNK_AA619412	AA619412

108753_at	0.00	0.00	0.00	0.00	-2.11	0.00	UNK_AW048441	AW048441
108770_at	0.00	0.00	0.00	0.00	-2.36	-1.57	UNK_AW124553	AW124553
108855_at	0.00	0.00	0.00	0.00	-5.20	0.00	UNK_AI647526	AI647526
109016_at	0.00	-1.69	-1.87	0.00	-3.06	-1.74	UNK_AI891634	AI891634
109047_at	0.00	0.00	0.00	0.00	-2.25	0.00	UNK_AI850557	AI850557
109124_at	0.00	0.00	0.00	0.00	-2.11	0.00	UNK_AW125343	AW125343
109348_at	0.00	0.00	0.00	0.00	-2.06	0.00	UNK_AI850333	AI850333
109361_at	0.00	-1.38	0.00	0.00	-2.31	-1.38	UNK_AA170632	AA170632
109386_at	0.00	0.00	-4.41	0.00	0.00	0.00	UNK_AA614943	AA614943
109390_at	0.00	-1.75	0.00	0.00	-2.84	-1.53	UNK_AW049308	AW049308
109415_at	0.00	0.00	0.00	0.00	0.00	-2.85	UNK_AI646948	AI646948
109570_at	0.00	0.00	0.00	0.00	-2.02	0.00	UNK_AA763178	AA763178
109575_at	0.00	0.00	0.00	0.00	-2.11	0.00	UNK_AI155995	AI155995
109655_at	0.00	-1.68	-1.90	0.00	-2.13	-1.65	UNK_W08276	W08276
109662_at	0.00	0.00	0.00	0.00	-2.84	0.00	UNK_AW122695	AW122695
109681_at	0.00	0.00	0.00	0.00	-2.17	-1.60	UNK_AI838049	AI838049
109738_at	0.00	0.00	0.00	0.00	-3.12	-1.76	UNK_AI099014	AI099014
109755_at	0.00	0.00	0.00	0.00	-2.03	0.00	UNK_AW047377	AW047377
109773_at	0.00	0.00	-2.04	0.00	0.00	0.00	UNK_AI852349	AI852349
109820_f_at	0.00	0.00	0.00	0.00	-2.03	0.00	UNK_AI840770	AI840770
109938_at	0.00	-1.55	-1.73	0.00	-2.46	-1.92	UNK_AA986399	AA986399
109955_at	0.00	0.00	0.00	0.00	-2.04	-1.73	UNK_AW122907	AW122907
109958_at	0.00	-1.50	0.00	0.00	-2.36	-1.91	UNK_AI503400	AI503400
110069_at	0.00	-1.80	0.00	0.00	-2.21	0.00	UNK_AW123500	AW123500
110092_at	0.00	0.00	0.00	0.00	-2.07	-1.74	UNK_AW050361	AW050361
110096_at	0.00	0.00	0.00	0.00	-1.54	-2.02	UNK_AA718224	AA718224
110122_at	0.00	-1.49	0.00	0.00	-2.59	-1.94	UNK_AA762771	AA762771
110140_f_at	0.00	0.00	0.00	0.00	-2.59	0.00	UNK_AW060592	AW060592
110286_at	0.00	-1.78	0.00	0.00	-2.53	0.00	UNK_AI194762	AI194762
110290_at	0.00	0.00	0.00	0.00	0.00	-3.55	UNK_AW122616	AW122616
110292_at	0.00	0.00	0.00	0.00	-2.79	0.00	D9UCLA2	AI839742
110361_at	0.00	-1.63	-1.39	0.00	-3.08	-1.93	UNK_AI839531	AI839531
110442_at	0.00	0.00	0.00	0.00	-2.09	-1.65	UNK_AA960476	AA960476
110529_at	0.00	0.00	0.00	0.00	-2.21	-1.70	UNK_AI594683	AI594683
110644_s_at	0.00	-1.12	-5.38	0.00	0.00	0.00	UNK_AI593562	AI593562
110673_at	0.00	0.00	0.00	0.00	-2.03	0.00	UNK_W53698	W53698
110755_at	0.00	0.00	-2.59	0.00	-1.61	0.00	UNK_AI842126	AI842126
110757_at	0.00	0.00	0.00	0.00	-2.17	-1.85	UNK_AI847218	AI847218
110770_at	0.00	0.00	0.00	0.00	-2.06	0.00	UNK_AW045392	AW045392
110812_at	0.00	0.00	0.00	0.00	-2.87	-1.60	UNK_AI836721	AI836721
110826_at	0.00	0.00	-1.80	0.00	-2.02	-1.66	UNK_AW122152	AW122152
110972_at	0.00	0.00	0.00	-1.92	-2.38	-1.71	UNK_AI848760	AI848760
111305_at	0.00	-1.67	0.00	0.00	-2.84	-1.80	UNK_AW121459	AW121459
111359_at	0.00	-1.57	0.00	0.00	-3.83	-1.58	UNK_AW108291	AW108291
111382_at	0.00	0.00	0.00	0.00	-2.03	0.00	UNK_AI835341	AI835341
111431_at	0.00	-1.91	-1.68	0.00	-4.69	-1.78	UNK_AI836555	AI836555
111445_at	0.00	0.00	0.00	0.00	-2.41	-1.61	UNK_AW046417	AW046417
111517_at	0.00	0.00	0.00	0.00	-2.09	0.00	UNK_AA983096	AA983096
111548_g_at	0.00	0.00	0.00	0.00	-2.90	-2.00	UNK_AI851666	AI851666
111613_at	0.00	-1.36	0.00	0.00	-2.33	-1.44	UNK_AW228205	AW228205
111689_at	0.00	0.00	0.00	0.00	-2.18	0.00	UNK_AW060751	AW060751
111690_at	0.00	0.00	0.00	0.00	-2.27	0.00	UNK_AW125187	AW125187
111947_at	0.00	0.00	0.00	0.00	-2.29	0.00	UNK_AA789365	AA789365
112029_at	0.00	0.00	0.00	0.00	-2.61	-1.65	UNK_AA821545	AA821545
112063_at	0.00	0.00	0.00	0.00	-2.86	0.00	UNK_AA420218	AA420218
112073_at	0.00	0.00	0.00	0.00	-3.03	0.00	UNK_AA242716	AA242716
112081_at	0.00	0.00	0.00	0.00	-2.25	-1.64	UNK_AI510428	AI510428
112220_at	0.00	0.00	-2.37	0.00	0.00	0.00	UNK_AA763894	AA763894
112318_at	0.00	0.00	0.00	0.00	-2.38	-1.55	UNK_AW122090	AW122090

112336_at	0.00	-2.56	0.00	0.00	0.00	0.00	UNK_AI854546	AI854546
112352_at	0.00	0.00	0.00	0.00	-2.08	0.00	UNK_AI841571	AI841571
112363_at	0.00	0.00	0.00	0.00	-3.06	-1.80	UNK_AW048194	AW048194
112381_at	0.00	-1.69	-2.32	0.00	0.00	0.00	UNK_AA863867	AA863867
112398_at	0.00	0.00	0.00	0.00	-4.67	0.00	UNK_AW045591	AW045591
112406_at	0.00	0.00	0.00	0.00	-2.71	-1.61	UNK_AI851470	AI851470
112415_at	0.00	0.00	0.00	0.00	-2.06	-1.58	UNK_AI604376	AI604376
112432_at	0.00	0.00	0.00	0.00	-2.38	0.00	UNK_AW045567	AW045567
112668_at	0.00	0.00	0.00	0.00	-2.48	0.00	UNK_AW261533	AW261533
112722_at	0.00	0.00	0.00	0.00	0.00	-2.59	UNK_AW124381	AW124381
112820_at	0.00	-1.53	0.00	0.00	-3.27	-1.49	UNK_AW045244	AW045244
112920_at	0.00	0.00	0.00	0.00	-7.87	0.00	UNK_AW125065	AW125065
112947_at	0.00	0.00	0.00	0.00	-3.08	-1.87	UNK_AA693298	AA693298
113012_at	0.00	-1.77	-1.53	0.00	-4.20	-1.84	UNK_AI846919	AI846919
113210_at	0.00	-1.92	0.00	0.00	-2.72	-0.66	UNK_AI841042	AI841042
113232_at	0.00	0.00	0.00	0.00	-2.36	0.00	UNK_AI841061	AI841061
113314_at	0.00	0.00	0.00	0.00	-2.73	-1.77	UNK_AI840767	AI840767
113318_at	0.00	0.00	0.00	0.00	-2.72	-1.78	UNK_AW261686	AW261686
113330_at	0.00	0.00	0.00	0.00	-2.01	-0.45	UNK_AI527630	AI527630
113565_at	0.00	0.00	0.00	0.00	-2.22	0.00	UNK_AW049089	AW049089
113604_at	0.00	-1.61	0.00	0.00	-2.40	0.00	UNK_AI847956	AI847956
113638_at	0.00	0.00	0.00	0.00	-2.45	-1.83	UNK_AW045993	AW045993
113715_at	0.00	-1.98	0.00	0.00	-2.01	-1.62	UNK_AA822301	AA822301
113785_at	0.00	0.00	-1.72	0.00	-2.43	-1.66	UNK_AI850504	AI850504
113901_at	0.00	0.00	0.00	0.00	-1.89	-2.14	UNK_AI593827	AI593827
113938_at	0.00	0.00	0.00	0.00	-4.11	0.00	UNK_AI842866	AI842866
113985_at	-2.17	0.00	0.00	0.00	0.00	0.00	UNK_AI838258	AI838258
113986_at	0.00	-1.99	0.00	0.00	-2.92	0.00	UNK_AI510303	AI510303
113990_at	0.00	0.00	0.00	0.00	-2.03	0.00	UNK_AA763276	AA763276
113998_at	0.00	0.00	0.00	0.00	0.00	-2.00	UNK_AA416235	AA416235
114069_at	0.00	0.00	0.00	0.00	-2.72	-1.86	UNK_AI844797	AI844797
114093_at	0.00	0.00	0.00	0.00	-2.00	0.00	UNK_AI852806	AI852806
114143_at	0.00	0.00	0.00	0.00	-2.11	0.00	UNK_AI853600	AI853600
114296_at	0.00	0.00	0.00	0.00	-2.72	-1.42	UNK_AA823920	AA823920
114316_at	0.00	0.00	0.00	0.00	-2.92	-1.69	UNK_AI605358	AI605358
114392_at	0.00	0.00	0.00	0.00	-2.85	0.00	UNK_AW120619	AW120619
114416_at	0.00	0.00	0.00	0.00	0.00	-3.51	UNK_AW045985	AW045985
114418_at	0.00	0.00	0.00	0.00	-2.38	0.00	UNK_AI854454	AI854454
114476_at	0.00	0.00	0.00	0.00	-2.89	0.00	UNK_AI482420	AI482420
114478_at	0.00	0.00	0.00	0.00	0.00	-3.17	UNK_AA061949	AA061949
114706_at	0.00	0.00	0.00	0.00	-2.32	-1.36	UNK_AW049085	AW049085
114752_at	0.00	-2.01	0.00	0.00	0.00	2.84	UNK_AI843572	AI843572
114794_at	0.00	-1.73	0.00	0.00	-2.33	-1.39	UNK_AA693185	AA693185
114982_at	0.00	-1.59	0.00	0.00	-3.53	-1.98	UNK_AA959852	AA959852
115077_f_at	0.00	0.00	0.00	0.00	-2.03	0.00	DBT	AA896722
115078_r_at	0.00	0.00	0.00	0.00	-2.52	0.00	DBT	AA896722
115106_at	0.00	-1.49	0.00	0.00	-2.69	-1.92	UNK_AI851210	AI851210
115169_at	0.00	0.00	0.00	0.00	-2.15	0.00	UNK_AW047351	AW047351
115323_at	0.00	0.00	-1.34	0.00	-2.07	-1.72	UNK_AA107507	AA107507
115370_at	0.00	0.00	0.00	0.00	-2.38	0.00	UNK_AI527642	AI527642
115376_at	0.00	0.00	0.00	0.00	-2.23	0.00	UNK_AI850511	AI850511
115428_at	0.00	0.00	-1.95	0.00	-3.82	0.00	UNK_AA673260	AA673260
115437_at	0.00	-1.66	0.00	0.00	-2.21	-1.37	UNK_AW049924	AW049924
115545_at	0.00	0.00	0.00	0.00	-2.29	0.00	UNK_AA940371	AA940371
115629_at	0.00	0.00	0.00	0.00	0.00	-3.06	UNK_AA183896	AA183896
115640_at	0.00	0.00	0.00	0.00	-2.88	-0.66	UNK_AI451541	AI451541
115686_at	0.00	0.00	0.00	0.00	-3.34	0.00	UNK_AI853521	AI853521
115845_at	0.00	0.00	0.00	0.00	-2.24	-1.49	UNK_AW107813	AW107813
115847_i_at	0.00	0.00	0.00	0.00	-2.07	-1.59	UNK_AI327072	AI327072

116046_at	0.00	0.00	0.00	0.00	-2.42	0.00	UNK_AI848153	AI848153
116151_at	0.00	0.00	-2.09	0.00	0.00	0.00	UNK_AI845734	AI845734
116152_at	0.00	0.00	0.00	0.00	-5.30	-1.89	UNK_AI840320	AI840320
116263_at	0.00	0.00	0.00	0.00	-2.20	-1.49	UNK_AW060609	AW060609
116349_at	0.00	0.00	0.00	0.00	-2.01	0.00	UNK_AI155885	AI155885
116406_at	0.00	0.00	0.00	0.00	0.00	-2.81	UNK_AW050231	AW050231
116438_at	0.00	0.00	0.00	0.00	0.00	-2.92	UNK_AI853912	AI853912
116466_at	0.00	0.00	0.00	0.00	-2.94	-1.80	UNK_AI591541	AI591541
116661_at	0.00	0.00	0.00	0.00	-2.81	0.00	UNK_AI594516	AI594516
116771_at	0.00	0.00	0.00	0.00	-2.16	-1.56	UNK_AI843862	AI843862
116856_at	0.00	0.00	0.00	0.00	-2.08	0.00	UNK_AW122439	AW122439
116887_at	0.00	0.00	0.00	0.00	-2.49	0.00	UNK_AI848169	AI848169
116919_f_at	0.00	0.00	0.00	0.00	-3.43	-1.62	UNK_AI837430	AI837430
116949_at	0.00	0.00	0.00	0.00	-2.30	-1.95	UNK_AI835398	AI835398
116967_at	0.00	0.00	0.00	0.00	-2.74	-1.58	UNK_AI851900	AI851900
116975_at	0.00	0.00	0.00	0.00	0.00	-2.24	UNK_AI848908	AI848908
117008_at	0.00	0.00	0.00	0.00	-2.41	0.00	UNK_AI836364	AI836364
117080_at	0.00	0.00	0.00	0.00	-4.41	-1.77	UNK_AW046827	AW046827
117107_at	0.00	-1.73	-1.97	0.00	-3.77	-1.76	UNK_AI837768	AI837768
117123_at	0.00	-2.18	0.00	0.00	-1.51	0.00	UNK_AI840704	AI840704
117125_at	0.00	0.00	-0.03	0.00	-3.36	-0.88	UNK_AI835705	AI835705
117178_at	0.00	0.00	0.00	0.00	-2.32	-1.81	UNK_AI844448	AI844448
117206_at	0.00	0.00	0.00	0.00	-5.29	0.00	UNK_AW122028	AW122028
117213_at	0.00	-1.74	0.00	0.00	-3.01	-1.60	UNK_AI850929	AI850929
117307_at	0.00	0.00	0.00	0.00	-3.93	0.00	UNK_AI844588	AI844588
117308_at	0.00	0.00	0.00	0.00	-2.09	0.00	UNK_AI835357	AI835357
128879_f_at	0.00	0.00	0.00	0.00	-3.24	0.00	UNK_AI838074	AI838074
129016_f_at	0.00	0.00	0.00	0.00	-1.50	-2.09	UNK_AI596402	AI596402
129176_at	0.00	0.00	0.00	0.00	0.00	-13.63	UNK_AI607324	AI607324
129231_at	0.00	-5.11	0.00	0.00	0.00	0.00	UNK_AW046840	AW046840
129306_r_at	0.00	0.00	0.00	0.00	-2.42	-1.86	UNK_AI606549	AI606549
129582_at	0.00	0.00	0.00	0.00	-2.32	-1.74	UNK_AI465103	AI465103
130312_at	0.00	0.00	0.00	0.00	-1.96	-2.85	UNK_AW215796	AW215796
130512_at	0.00	-1.69	0.00	0.00	-2.50	-1.87	UNK_AI848603	AI848603
130696_f_at	0.00	0.00	0.00	-3.94	0.00	0.00	UNK_AW210623	AW210623
130730_f_at	0.00	0.00	0.00	0.00	-1.91	-2.09	UNK_AA270325	AA270325
132118_at	0.00	-1.73	0.00	-2.16	-1.93	-1.94	UNK_AI642706	AI642706
133171_at	0.00	-2.00	-1.80	0.00	0.00	0.00	UNK_AA683786	AA683786
133759_at	0.00	0.00	0.00	0.00	-2.61	0.00	UNK_AI480951	AI480951
133886_at	0.00	0.00	0.00	0.00	-4.76	0.00	UNK_AA168908	AA168908
134047_at	0.00	-1.88	0.00	0.00	-2.17	-1.74	UNK_AW123320	AW123320
134281_at	0.00	0.00	0.00	0.00	-2.51	0.00	UNK_AI551165	AI551165
134622_f_at	-2.30	0.00	0.00	0.00	0.00	0.00	UNK_AI641962	AI641962
134778_at	0.00	-1.98	-1.91	0.00	-2.80	-1.87	UNK_AI666678	AI666678
135643_at	0.00	-2.73	0.00	0.00	0.00	0.00	UNK_AA396310	AA396310
135691_at	0.00	-1.77	0.00	0.00	-2.36	-1.46	UNK_AA882067	AA882067
136174_at	0.00	0.00	-1.68	0.00	-2.11	-1.50	UNK_AW048956	AW048956
136545_at	0.00	-4.44	-1.77	0.00	-1.82	0.00	UNK_AA982069	AA982069
136719_at	0.00	0.00	0.00	0.00	-2.50	0.00	UNK_AI847908	AI847908
137973_at	0.00	-1.94	-1.65	0.00	-3.24	-1.85	UNK_AI843877	AI843877
137979_at	0.00	-2.19	0.00	0.00	0.00	0.00	UNK_AI848070	AI848070
138060_at	0.00	0.00	0.00	0.00	-2.00	0.00	UNK_AW122571	AW122571
138086_f_at	0.00	0.00	0.00	0.00	-1.73	-2.25	UNK_AW122816	AW122816
138556_at	0.00	0.00	0.00	0.00	0.00	-2.27	UNK_AI874931	AI874931
139522_at	0.00	-1.48	0.00	0.00	-2.07	-1.56	UNK_AW046420	AW046420
139980_g_at	0.00	0.00	0.00	0.00	-3.05	-1.67	UNK_AI450646	AI450646
140519_at	0.00	0.00	0.00	0.00	-2.66	-1.97	UNK_AI642378	AI642378
140861_at	0.00	-2.29	0.00	0.00	-1.43	0.00	UNK_AI645591	AI645591
104962_at	0.00	0.00	0.00	0.00	0.78	-3.35	AA450473	AA450473

93316_at	0.00	0.00	0.00	0.00	-2.00	0.00	UNK_AB017026	AB017026
97172_s_at	0.00	0.00	0.00	0.00	-2.07	0.00	ABCC9	D86037
95425_at	0.00	0.00	0.00	0.00	-2.24	0.00	acetyl-Coenzyme A dehydrogenase, long-chain; Acadl	U21489
92581_at	0.00	0.00	-1.93	0.00	-2.49	0.00	acetyl-Coenzyme A dehydrogenase, medium chain; Acadm	U07159
106070_at	0.00	0.00	-3.56	0.00	-4.60	0.00	UNK_AI854239	AI854239
104650_at	0.00	0.00	0.00	0.00	0.00	-8.36	acetylcholinesterase; Ache	X56518
101515_at	0.00	0.00	0.00	0.00	-2.32	0.00	acyl-Coenzyme A oxidase; Acox-pending	AF006688
101028_i_at	0.00	-1.72	-3.47	0.00	-3.72	-2.05	actin, alpha, cardiac; Actc1	M15501
93903_at	0.00	0.00	0.00	0.00	-3.07	0.00	activin receptor IIB; Acvr2b	M84120
99671_at	0.00	-1.93	-2.01	0.00	0.00	1.51	adipsin; Adn	X04673
98999_at	0.00	0.00	0.00	0.00	-2.64	-1.88	ADSL	AA606587
98435_at	0.00	0.00	0.00	0.00	-2.43	-2.03	*adenylosuccinate* synthetase 1, muscle; Adss1	M74495
111708_at	0.00	0.00	0.00	0.00	-2.33	-1.94	AF180471	AA709944
97279_at	0.00	0.00	0.00	0.00	-2.14	0.00	UNK_AI837615	AI837615
110392_at	0.00	0.00	0.00	0.00	-2.20	0.00	UNK_AA789854	AA789854
112429_at	-1.97	-1.95	-1.77	0.00	-2.77	0.00	UNK_AI462012	AI462012
112387_at	0.00	-2.45	0.00	0.00	-3.22	-2.31	UNK_AI747215	AI747215
99521_at	0.00	0.00	0.00	0.00	-2.53	0.00	AK4	AB020239
92768_s_at	0.00	0.00	-2.85	-2.29	0.00	0.00	aminolevulinic acid synthase 2, erythroid; Alas2	M15268
93500_at	0.00	0.00	0.00	0.00	-2.08	0.00	0	M63245
100068_at	0.00	-1.88	0.00	0.00	-3.32	-1.91	alcohol dehydrogenase family 1, subfamily A2; Aldh1a2	M74570
101489_at	0.00	0.00	0.00	0.00	-2.09	-2.05	AMD1	D12780
100323_at	0.00	0.00	-1.91	0.00	-2.12	0.00	AMD2	Z23077
100324_g_at	0.00	0.00	0.00	0.00	-2.21	-1.84	AMD2	Z23077
101058_at	0.00	0.00	-2.85	0.00	-2.87	-2.06	AMY1	J00356
100440_f_at	0.00	0.00	0.00	0.00	-3.30	-2.28	ANK1	U76758
100441_s_at	0.00	0.00	0.00	0.00	-5.39	-2.20	ANK1	X69064
100439_i_at	0.00	0.00	0.00	0.00	-2.65	-1.95	ANK1	U76758
98476_at	0.00	0.00	-1.74	0.00	-2.10	0.00	ANK3	L40631
98477_s_at	0.00	-1.84	0.00	0.00	-3.34	-1.89	ankyrin 3, epithelial; Ank3	L40632
97786_at	-1.75	0.00	0.00	0.00	-2.14	-1.51	UNK_AJ011118	AJ011118
97235_f_at	0.00	-1.80	-2.29	0.00	-3.50	0.00	APOBEC2	AW124988
93592_at	-1.50	-3.36	0.00	0.00	0.00	0.00	*apolipoprotein D*; Apod	X82648
109808_at	0.00	0.00	0.00	0.00	-3.03	0.00	APOE	AI504617
102704_at	-0.92	-4.95	-3.29	-4.01	-5.56	-3.77	aquaporin 4; Aqp4	U88623
102703_s_at	0.00	-2.91	0.00	0.00	-3.94	-2.23	AQP4	U48398
102382_at	0.00	0.00	0.00	0.00	0.00	-2.46	ARNTL	AB014494
99481_at	0.00	0.00	-1.98	0.00	-2.90	-2.33	UNK_AI839697	AI839697
93664_at	0.00	0.00	0.00	0.00	0.00	-2.07	ATP1B2	X16645
99570_s_at	0.00	-2.68	-1.76	-2.81	-1.98	0.00	ATP2A2	AF029982

103699_i_at	0.00	-2.48	-3.08	0.00	-3.36	-2.40	UNK_AI646638	AI646638
96035_at	0.00	0.00	-2.13	0.00	-2.59	-1.68	branched chain ketoacid dehydrogenase E1, alpha polypeptide; Bckdha	L47335
102302_at	0.00	0.00	-1.89	0.00	-2.21	0.00	BCKDHB	L16992
103015_at	0.00	0.00	0.00	0.00	-2.04	0.00	B-cell leukemia/lymphoma 6; Bcl6	U41465
93836_at	0.00	-2.58	-2.53	0.00	-3.95	-1.74	BNIP3	AF041054
101903_at	0.00	0.00	0.00	0.00	-3.93	-2.66	CD8beta opposite strand; Bop	U76371
94815_at	0.00	-1.91	-2.05	0.00	-3.33	0.00	2,3-bisphosphoglycerate mutase; Bpgm	X13586
113861_at	0.00	0.00	0.00	0.00	-2.15	-1.61	BVES-PENDING	AI152383
101128_at	0.00	0.00	0.00	0.00	-2.93	-2.12	calcium channel, voltage-dependent, L type, alpha 1S subunit; Cacna1s	L06234
99812_at	0.00	-1.79	0.00	0.00	-2.40	-2.09	calpain 3; Capn3	X92523
99813_g_at	0.00	0.00	0.00	0.00	-2.54	-2.11	calpain 3; Capn3	X92523
98079_at	-2.36	-4.93	0.00	0.00	-13.32	-6.68	CAR14	AB005450
92642_at	0.00	0.00	-2.16	0.00	-2.62	5.27	CAR2	M25944
100600_at	0.00	0.00	0.00	0.00	-2.40	-2.04	CD24A	M58661
93332_at	0.00	0.00	0.00	0.00	-2.65	-1.74	CD36 antigen; Cd36	L23108
101516_at	0.00	0.00	-2.01	0.00	0.00	0.00	CD59	U60473
104743_at	0.00	0.00	0.00	0.00	-2.26	-2.14	UNK_AB022100	AB022100
95471_at	0.00	-2.68	-2.76	0.00	2.10	1.92	cyclin-dependent kinase inhibitor 1C (P57); Cdkn1c	U22399
104209_at	0.00	0.00	0.00	0.00	-6.63	-3.70	CHRP	AI847016
99994_at	0.00	0.00	-2.89	0.51	-3.44	0.00	CIDEA	AF041376
94463_at	0.00	0.00	0.00	0.00	-5.15	0.00	chloride channel 3; Clcn3	X78874
94464_at	0.00	-1.75	0.00	0.00	-2.12	-1.59	CLCN3	AF029347
94465_g_at	0.00	0.00	0.00	0.00	-2.01	-1.32	CLCN3	AF029347
92322_at	0.00	0.00	-2.94	-1.65	-2.57	0.00	cathelin-like protein; Cnlp	X94353
93582_at	0.00	0.00	0.00	0.00	-2.10	0.00	COQ7	AF080580
102749_at	0.00	0.00	-1.45	0.00	-2.37	-1.32	COX7A1	AF037370
113828_at	0.00	-2.35	-2.07	0.00	-4.31	-2.24	CPT1B	AA189179
102951_at	0.00	0.00	0.00	0.00	0.00	-2.03	CRADD	AJ224738
103646_at	0.00	0.00	-1.75	0.00	-2.43	-1.81	carnitine acetyltransferase; Crat	X85983
99065_at	0.00	0.00	0.00	-2.08	0.00	0.00	casein kappa; Csnk	M10114
97336_at	0.00	-2.65	0.00	0.00	0.00	2.12	UNK_AJ131851	AJ131851
98132_at	0.00	0.00	0.00	0.00	-3.97	0.00	cytochrome c, somatic; Cycs	X01756
93996_at	0.00	-4.02	-5.63	-4.92	-3.73	0.00	CYP2E1	X01026
94526_at	0.00	0.00	0.00	0.00	-2.34	0.00	UNK_AI848453	AI848453
96757_at	0.00	0.00	-2.06	0.00	-3.05	-1.95	D10JHU81E	AI852165
109645_at	0.00	0.00	0.00	0.00	-2.03	-1.59	UNK_AW123377	AW123377

113324_at	0.00	0.00	0.00	0.00	-2.47	0.00	UNK_AI121830	AI121830
96803_at	0.00	0.00	0.00	0.00	-2.32	0.00	UNK_AW210370	AW210370
96346_at	0.00	-1.46	-2.12	0.00	2.45	5.93	D18UCLA3	AI854020
133703_at	0.00	0.00	0.00	0.00	-2.52	-2.07	UNK_AI462192	AI462192
95594_at	0.00	-2.01	-2.26	0.00	-2.86	-2.01	UNK_AI847486	AI847486
93614_at	0.00	0.00	0.00	0.00	-4.05	-4.34	UNK_AA600647	AA600647
99959_at	0.00	0.00	0.00	0.00	-2.42	0.00	UNK_AW061337	AW061337
97397_at	0.00	0.00	0.00	0.00	-2.35	-1.50	UNK_AI848344	AI848344
113212_at	0.00	0.00	0.00	0.00	-4.09	-1.85	UNK_AI848538	AI848538
102859_at	0.00	-1.90	0.00	0.00	-2.02	-1.80	UNK_AW121304	AW121304
96112_at	0.00	0.00	0.00	0.00	-2.15	0.00	UNK_AI851178	AI851178
112421_at	0.00	-2.29	0.00	0.00	-6.07	-3.49	UNK_AI838528	AI838528
103617_at	0.00	0.00	0.00	0.00	-2.42	0.00	decay accelerating factor 1; Daf1	D63679
98966_at	0.00	0.00	0.00	0.00	-2.58	-0.74	dihydrolipoamide branched chain transacylase E2; Dbt	L42996
98527_at	0.00	-2.22	0.00	0.00	-3.37	-2.02	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Dci	Z14050
95478_at	0.00	0.00	0.00	0.00	-2.07	-1.81	DEB1	AW124231
99485_at	0.00	0.00	0.00	0.00	-2.08	0.00	DFFA	AB009376
108255_at	0.00	0.00	0.00	0.00	-2.29	-2.60	DUSP13	AA144705
100311_f_at	0.00	0.00	-2.37	0.00	0.00	0.00	EAR1	U72032
103240_f_at	0.00	0.00	-3.40	0.00	0.00	0.00	EAR3	AF017258
93754_at	0.00	0.00	0.00	0.00	-2.05	0.00	enoyl coenzyme A hydratase 1, peroxisomal; Ech1	AF030343
102774_at	0.00	-1.77	0.00	0.00	-2.89	-1.98	epidermal growth factor; Egf	V00741
94353_at	0.00	0.00	0.00	0.00	0.00	-2.24	eukaryotic translation initiation factor 4E binding protein 2; Eif4ebp2	U75530
93051_at	0.00	-2.61	0.00	0.00	-2.14	0.00	EPHX2	Z37107
101538_i_at	0.00	-4.79	-3.78	0.00	-7.47	-1.63	ES1	AW226939
101539_f_at	0.00	-3.93	-3.37	0.00	-7.31	0.00	ES1	AW226939
103964_at	0.00	-1.62	-1.63	0.00	-2.22	0.00	estrogen related receptor, alpha; Esrra	U85259
115969_at	0.00	0.00	0.00	0.00	-2.50	0.00	EXTL1	AI850861
94214_at	0.00	-2.71	0.00	0.00	-3.30	0.00	FABP3	X14961
94507_at	0.00	0.00	0.00	0.00	-2.62	0.00	fatty acid Coenzyme A ligase, long chain 2; Facl2	U15977
98575_at	0.00	-1.34	-3.15	-2.39	-3.33	0.00	fatty acid synthase; Fasn	X13135
100928_at	-4.16	0.00	0.00	2.21	-0.01	19.58	fibulin 2; Fbln2	X75285
97379_at	-0.89	-3.22	-4.99	0.00	-7.21	-4.72	fructose bisphosphatase 2; Fbp2	D42083

97518_at	0.00	-3.76	-2.66	0.00	-2.48	-1.86	farnesyl diphosphate farnesyl transferase 1; Fdft1	D29016
92587_at	0.00	0.00	0.00	0.00	-2.01	0.00	ferredoxin 1; Fdx1	L29123
97213_at	0.00	-2.01	-2.18	0.00	-3.49	-2.34	FEM1A	AF064447
100494_at	0.00	0.00	0.00	0.00	-3.74	0.00	FGF1	M30641
103995_at	0.00	0.00	0.00	0.00	-2.00	-2.32	FGFBP1	AF065441
102366_at	0.00	0.00	-5.06	-3.75	0.00	2.31	UNK_AA718169	AA718169
101991_at	0.00	-2.61	0.00	0.00	-1.59	1.77	flavin containing monooxygenase 1; Fmo1	D16215
104607_at	0.00	0.00	-1.82	0.00	-2.08	-1.72	UNK_AF093624	AF093624
99121_at	0.00	0.00	0.00	0.00	-2.20	0.00	fragile X mental retardation gene, autosomal homolog; Fxr1h	X90875
97430_at	0.00	-2.17	0.00	0.00	-3.62	-2.00	G6PT1	AF080469
104616_g_at	0.00	0.00	0.00	0.00	-3.11	0.00	galactose-1-phosphate uridyl transferase; Galt	M96265
102967_at	0.00	0.00	0.00	-1.64	-2.62	-2.68	GDAP1	Y17850
92592_at	0.00	0.00	0.00	0.00	-3.62	-2.07	GDC1	M25558
97155_at	-1.62	0.00	0.00	0.00	-4.30	-2.94	myostatin; Mstn	U84005
98984_f_at	0.00	0.00	0.00	0.00	-5.39	-2.75	glycerol phosphate dehydrogenase 1, mitochondrial; Gdm1	D50430
99107_at	0.00	-2.02	0.00	0.00	-1.80	0.00	GHR	M31680
102060_at	0.00	-2.08	0.00	0.00	-1.92	-1.63	GOLGA4	AF051357
100573_f_at	0.00	-1.98	-1.95	0.00	-2.35	-1.80	GPI1	M14220
113915_at	0.00	-2.92	-3.65	-4.26	-4.95	-3.03	UNK_AI226254	AI226254
93750_at	0.00	-2.13	-2.15	0.00	-1.75	0.00	gelsolin; Gsn	J04953
112869_at	0.00	0.00	0.00	0.00	-2.44	-2.45	GSNPAT-PENDING	AI852572
96085_at	0.00	0.00	0.00	0.00	0.00	-2.36	GSTA4	L06047
93543_f_at	0.00	0.00	-1.85	0.00	-2.20	0.00	GSTM1	J03952
102094_f_at	0.00	0.00	0.00	0.00	-3.22	-1.46	GSTM1	AI841270
95445_at	0.00	0.00	0.00	0.00	-1.96	-2.10	GUKMI1	AW124194
100597_at	0.00	0.00	0.00	0.00	-2.22	0.00	GYG1	AW049730
98496_at	0.00	-2.01	0.00	0.00	-2.49	-1.83	GYS3	U53218
95485_at	0.00	0.00	-1.89	0.00	-2.61	0.00	hydroxylacyl-Coenzyme A dehydrogenase-dehydrogenase; Hadh	D29639
94781_at	-1.29	-1.94	-2.84	-2.71	-1.65	0.00	hemoglobin alpha, adult chain 1; Hba-a1	V00714
103534_at	-1.77	-1.81	-3.81	0.00	-2.23	1.56	hemoglobin, beta adult minor chain; Hbb-b2	V00722
94375_at	0.00	0.00	0.00	0.00	-2.10	-1.94	hexokinase 2; Hk2	Y11666
92568_at	0.00	0.00	0.00	0.00	-1.92	-2.02	house-keeping protein 1; Hkp1	M74555
102714_at	0.00	0.00	0.00	0.00	-1.87	-2.08	HSC70T	L27086

97867_at	0.00	-2.03	0.00	0.00	0.00	0.00	hydroxysteroid 11-beta dehydrogenase 1; Hsd11b1	X83202
102620_at	0.00	0.00	0.00	0.00	-7.64	-4.63	UNK_AF088983	AF088983
97914_at	0.00	0.00	0.00	0.00	-2.02	-1.92	heat shock protein, 74 kDa, A; Hspa9a	D17666
95693_at	0.00	-2.56	-2.35	0.00	-2.04	-1.82	isocitrate dehydrogenase 2 (NADP+), mitochondrial; Idh2	U51167
93029_at	0.00	0.00	0.00	0.00	-2.22	0.00	isocitrate dehydrogenase 3 (NAD+), gamma; Idh3g	U68564
103904_at	0.00	-2.69	-2.38	0.00	0.00	0.00	insulin-like growth factor binding protein 6; Igfbp6	X81584
96764_at	-2.18	0.00	4.23	4.92	2.47	10.03	UNK_AJ007971	AJ007971
110795_at	0.00	0.00	0.00	0.00	-2.27	0.00	JDP1-PENDING	AI852445
94193_at	0.00	0.00	-3.26	0.00	-3.75	-2.14	KCNA7	AF032099
98787_at	0.00	0.00	0.00	0.00	0.00	-4.22	potassium inwardly rectifying channel, subfamily J, member 11; Kcnj11	D50581
102849_at	0.00	0.00	-3.01	0.00	0.00	0.00	potassium inwardly-rectifying channel, subfamily J, member 8; Kcnj8	D88159
94379_at	0.00	-2.47	-1.93	0.00	-2.35	-2.21	kinesin heavy chain member 1B; Kif1b	D17577
93527_at	0.00	-2.06	-2.23	0.00	0.00	0.00	KLF9	Y14296
93528_s_at	0.00	-1.98	0.00	0.00	-2.51	0.00	KLF9	AI848050
94321_at	0.00	0.00	0.00	0.00	-2.29	0.00	keratin complex 1, acidic, gene 10; Krt1-10	V00830
97976_at	0.00	0.00	0.00	0.00	-2.24	0.00	kinectin 1; Ktn1	L43326
92366_at	0.00	-2.03	0.00	0.00	0.00	0.00	laminin, alpha 2; Lama2	U12147
101990_at	0.00	-3.06	-2.70	0.00	-3.72	-1.80	lactate dehydrogenase 2, B chain; Ldh2	X51905
96608_at	0.00	0.00	0.00	0.00	-2.42	0.00	lupus nephritis-associated peptide 1; Lnap1	AF023463
113140_at	0.00	0.00	0.00	0.00	-3.11	-2.24	LOC56046	AI846417
103090_at	0.00	0.00	0.00	0.00	0.00	-2.06	LOC56046	AI838742
99536_at	0.00	0.00	0.00	0.00	-2.79	-2.17	UNK_AB016080	AB016080
112850_at	0.00	-1.89	-1.68	0.00	-2.20	-2.12	UNK_AW121352	AW121352
101115_at	0.00	0.00	0.00	-2.20	-2.15	-0.12	lactotransferrin; Ltf	J03298
130772_at	0.00	-2.36	-2.24	0.00	0.00	0.00	LYNX1	AI838844
137205_f_at	0.00	0.00	0.00	0.00	-2.71	0.00	LYNX1	AI839851
102828_at	0.00	0.00	0.00	0.00	-2.31	-1.54	mitogen activated protein kinase kinase 6; Map2k6	U39066

102829_s_at	0.00	0.00	0.00	0.00	-2.06	0.00	MAP2K6	X97052
102431_at	0.00	0.00	0.00	0.00	-0.45	-2.09	MTAPT	M18775
102742_g_at	0.00	0.00	0.00	0.00	-1.89	-2.98	MTAPT	M18775
96311_at	0.00	-2.37	0.00	0.00	-3.29	-2.09	MBP	M11533
97282_at	-11.15	0.00	0.00	0.00	0.00	0.00	MELA	D10049
103838_at	0.00	0.00	0.00	0.00	-2.36	-1.98	MG29	AB010144
102061_at	0.00	-3.00	-3.32	-3.75	-5.64	-2.29	MLF1	AF100171
103622_at	-1.34	0.00	0.00	0.00	-2.19	-1.80	UNK_AW050255	AW050255
96348_at	0.00	-2.13	0.00	0.00	-2.20	0.00	UNK_AW121217	AW121217
101082_at	0.00	0.00	-2.34	0.00	-2.56	-1.12	MOD1	J02652
102096_f_at	0.00	0.00	-2.42	0.00	0.00	3.13	MUP1	AI255271
101909_f_at	0.00	0.00	-4.14	0.00	0.00	3.70	MUP3	M16357
100017_at	-1.56	0.00	0.00	0.00	-2.75	0.00	myosin-binding protein H; Mybph	U68267
97990_at	0.00	0.00	0.00	0.00	-2.28	0.00	myosin heavy chain 11, smooth muscle; Myh11	D85923
98616_f_at	0.00	-8.12	-2.13	-32.76	-4.63	-4.81	MYHCB	AJ223362
93050_at	0.00	-2.77	0.00	0.00	-2.91	-2.11	myosin light chain, phosphorylatable, cardiac ventricles; Mylpc	M91602
94122_at	7.47	3.44	2.58	0.00	-3.81	-1.94	MYOC	AF041335
92407_at	0.00	-1.90	0.00	0.00	-3.23	-2.03	MYOM1	AJ012072
102041_at	0.00	0.00	0.00	0.00	-2.53	-1.90	MYOM2	AJ001038
92876_at	0.00	0.00	0.00	0.00	-4.44	-2.04	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18 kDa); Ndufs4	AA590675
93006_at	0.00	0.00	0.00	0.00	-4.91	-2.79	NFIC	Y07693
96153_at	0.00	0.00	-4.66	-8.35	-10.04	-5.56	neutrophilic granule protein; Ngp	L37297
92824_at	0.00	0.00	0.00	0.00	-2.29	-1.91	NM23-M6	AF051942
99009_at	0.00	-2.54	0.00	0.00	-2.06	0.00	nicotinamide nucleotide transhydrogenase; Nnt	Z49204
98365_at	0.00	0.00	0.00	0.00	0.00	-2.02	nitric oxide synthase 1, neuronal; Nos1	D14552
102371_at	0.00	0.00	0.00	0.00	-3.52	-2.20	nuclear receptor subfamily 4, group A, member 1; Nr4a1	X16995
92362_at	0.00	0.00	0.00	0.00	0.00	-2.83	NTTP1	X95518
99549_at	0.00	-3.17	0.00	0.00	3.34	2.12	osteoglycin; Ogn	D31951
104479_at	0.00	0.00	0.00	0.00	-4.22	-5.06	purinergic receptor P2Y, G-protein coupled 2; P2ry2	L14751
113762_at	0.00	0.00	0.00	0.00	-2.71	0.00	UNK_AI510151	AI510151
96735_at	0.00	0.00	0.00	0.00	0.00	-2.76	UNK_AW049732	AW049732
93308_s_at	0.00	0.00	0.00	-1.80	-4.41	0.00	PCX	M97957
100489_at	0.00	0.00	0.00	0.00	0.00	-2.12	phosphodiesterase 7A; Pde7a	U68171
115211_at	0.00	0.00	0.00	0.00	-2.66	-1.52	PDHX	AA987055

103526_at	0.00	0.00	0.00	0.00	-3.17	-2.61	peptidyl arginine deiminase, type II; Pdi2	D16580
102049_at	-1.92	0.00	0.00	0.00	-2.30	0.00	PDK4	AJ001418
103297_at	0.00	0.00	-5.49	0.00	-5.13	-4.79	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1; Pfkfb1	X98848
93567_at	0.00	0.00	0.00	0.00	-2.14	-1.90	PFN2	AW122536
92599_at	0.00	0.00	0.00	0.00	-2.14	-1.47	PGAM2	AF029843
94733_at	0.00	-1.95	-2.18	-1.90	-2.98	-1.72	P glycoprotein 2; Pgy2	J03398
94855_at	0.00	0.00	0.00	0.00	-4.56	-3.15	prohibitin; Phb	X78682
92519_at	0.00	-2.02	-2.13	0.00	-2.66	-2.06	phosphorylase kinase alpha 1; Phka1	X74616
97094_at	0.00	0.00	-2.50	0.00	-5.08	-2.05	phosphorylase kinase gamma; Phkg	J03293
107109_at	0.00	0.00	0.00	0.00	-4.21	-2.18	PHRET1	AI835608
104431_at	0.00	0.00	0.00	0.00	-3.03	-1.83	protein kinase C, theta; Pkcq	D11091
98004_at	0.00	0.00	0.00	0.00	-2.53	-2.11	protein kinase inhibitor, alpha; Pkia	M63554
98005_at	0.00	0.00	0.00	0.00	-2.57	-1.86	PKIA	AW125442
113154_at	0.43	0.00	-2.71	-1.11	-2.08	2.44	UNK_AI854500	AI854500
96114_at	0.00	0.00	0.00	0.00	-2.25	0.00	UNK_AW122076	AW122076
93933_at	0.00	0.00	0.00	0.00	-2.41	-2.58	protein phosphatase 1, regulatory (inhibitor) subunit 5; Ppp1r5	U89924
97989_at	0.00	0.00	0.00	0.00	-2.59	-1.60	protein phosphatase 3, catalytic subunit, beta isoform; Ppp3cb	M81483
96256_at	0.00	0.00	0.00	0.00	-2.17	0.00	peroxiredoxin 3; Prdx3	M28723
97096_at	0.00	0.00	0.00	0.00	-5.20	-2.84	protein kinase, cAMP dependent regulatory, type II alpha; Prkar2a	J02935
100595_at	0.00	0.00	0.00	0.00	-2.33	0.00	PTP4A2	AF035644
101027_s_at	0.00	-1.93	0.00	0.00	-2.20	-1.52	PTTG1	AF069051
96720_f_at	0.00	0.00	0.00	0.00	-2.67	0.00	parvalbumin; Pva	X59382
104098_at	0.00	-2.59	-2.95	-3.60	-3.43	-2.09	peroxisomal membrane protein 2, 22 kDa; Pxmp2	L28835
92410_at	0.00	0.00	0.00	0.00	0.00	-2.59	RAD23a homolog (S. cerevisiae); Rad23a	X92410
104680_at	0.00	-2.27	-2.19	0.00	0.00	0.00	RAMP1	AJ250489
100562_at	0.00	0.00	0.00	0.00	-3.97	-3.48	UNK_AI846319	AI846319
99951_at	0.00	0.00	0.00	0.00	0.00	-4.08	RORC	AF019660
98464_at	0.00	0.00	0.00	0.00	-2.35	0.00	UNK_AW124196	AW124196
96296_at	0.00	0.00	0.00	0.00	-2.25	0.00	RPML7	AI843685
98007_at	0.00	-3.41	-2.82	-3.72	-3.18	-2.45	RPS6KA2	AJ131021

92237_at	0.00	0.00	0.00	0.00	-9.91	-5.35	retinoid X receptor gamma; Rxrg	X66225
103448_at	0.00	2.51	-4.75	-1.37	-6.47	3.81	S100 calcium binding protein A8 (calgranulin A); S100a8	M83218
103887_at	4.41	0.00	-8.99	-5.52	-6.50	5.43	S100 calcium-binding protein A9 (calgranulin B); S100a9	M83219
102763_at	0.00	0.00	0.00	0.00	-2.52	-1.62	UNK_AF064748	AF064748
102712_at	-3.84	2.96	4.98	8.61	4.23	0.00	serum amyloid A 3; Saa3	X03505
99665_at	0.00	0.00	-2.09	-2.05	-3.58	-2.00	special AT-rich sequence binding protein 1; Satb1	U05252
111448_f_at	0.00	-1.94	-1.73	0.00	-2.64	-1.81	SATB1	AI121993
111449_r_at	0.00	0.00	0.00	0.00	-2.19	0.00	SATB1	AI121993
103399_at	0.00	0.00	0.00	0.00	0.00	-2.01	SCML1	AI853225
102808_at	0.00	0.00	0.00	0.00	-2.21	-1.64	sodium channel, voltage-gated, type I, beta polypeptide; Scn1b	L48687
94140_at	0.48	2.44	-2.79	0.00	0.00	0.00	SCVR	M59446
92742_at	0.00	-4.88	0.00	0.00	-2.58	-1.69	SCYA11	U77462
98624_at	0.00	-1.98	-2.23	0.00	-2.88	-2.07	seb4 protein; Seb4	X75316
103395_at	0.00	0.00	0.00	0.00	-2.03	-1.79	SGCA	AF019564
101394_at	0.00	0.00	0.00	0.00	-2.25	0.00	SGCG	AB024922
96204_at	0.00	0.00	0.00	0.00	-2.53	0.00	SH3BGR	AJ239082
102208_at	0.00	-1.79	-2.13	0.00	-2.43	0.00	ST3GALVI	AI153959
99320_at	0.00	0.00	0.00	0.00	-2.62	0.00	sialyltransferase 8 (alpha 2, 8 sialytransferase) E; Siat8e	X98014
92722_f_at	0.00	0.00	0.00	0.00	-2.03	0.00	sine oculis-related homeobox 1 homolog (Drosophila); Six1	X80339
93000_g_at	-2.80	-2.40	0.00	0.00	0.00	0.00	SIX4	D50416
93001_at	-1.65	0.00	0.00	0.00	-2.44	0.00	sine oculis-related homeobox 4 homolog (Drosophila); Six4	D50418
102314_at	0.00	-2.97	0.00	0.00	-4.23	-2.74	solute carrier family 2 (facilitated glucose transporter), member 4; Slc2a4	M23383
109069_at	0.00	-2.82	-2.00	0.00	0.00	3.28	SLC39A1	AI255982
96926_at	-2.06	-2.87	-2.56	0.00	0.00	0.00	UNK_AA980164	AA980164
96042_at	0.00	0.00	0.00	0.00	-2.94	0.00	SOD2	L35528
92302_at	0.00	0.00	-1.87	0.00	-2.80	0.00	Son of sevenless homolog 2, (Drosophila); Sos2	Z11664
92726_at	0.00	0.00	0.00	0.00	-3.87	-2.50	SOX6	AJ010605
113125_at	0.00	0.00	0.00	0.00	-3.81	-2.03	UNK_AI851671	AI851671
100952_at	0.00	0.00	0.00	0.00	-2.38	-2.24	stromal interaction molecule 1; Stim1	U47323

92888_s_at	0.00	0.00	0.00	0.00	-2.62	-1.73	protein tyrosine phosphatase-like unspliced c-terminal product and spliced c-terminal end STYX; hStyxb	U34973
93501_f_at	0.00	0.00	0.00	0.00	-2.61	0.00	SUCLA2	AF058955
93502_r_at	0.00	0.00	0.00	0.00	-4.71	0.00	SUCLA2	AF058955
96268_at	0.00	0.00	0.00	0.00	-2.29	0.00	UNK_AI840979	AI840979
100587_f_at	0.00	0.00	0.00	0.00	-2.02	0.00	SUPT4H	AI843959
93994_at	0.00	0.00	0.00	0.00	-2.00	0.00	SYCP3	AW212131
102221_at	0.00	0.00	0.00	0.00	-2.28	-1.75	SYNGR1	AJ002306
100355_g_at	0.00	0.00	0.00	0.00	-2.24	-1.51	TBX14	AF013282
102256_at	0.00	0.00	0.00	0.00	-2.14	0.00	TBX15	AF041822
102344_s_at	0.00	-2.14	-2.56	-4.39	-4.38	-2.48	TCEA3	AI132239
97402_at	-2.80	-5.83	-4.24	-3.96	-4.97	-2.21	thioether S-methyltransferase; Temt	M88694
101964_at	0.00	0.00	-2.16	0.00	0.00	3.47	transketolase; Tkt	U05809
92224_at	0.00	-5.01	0.00	0.00	0.00	0.00	tetranectin (plasminogen-binding protein); Tna	X79199
101063_at	0.00	-3.19	0.00	0.00	0.00	-2.68	troponin C, cardiac/slow skeletal; Tncc	M29793
98561_at	0.00	-3.08	0.00	0.00	0.00	-2.24	UNK_AJ242874	AJ242874
93532_at	0.00	0.00	0.00	0.00	-2.52	0.00	troponin I, skeletal, fast 2; Tnni2	J04992
101383_at	0.00	-2.85	0.00	0.00	-1.69	-1.97	TNNT1	AJ131711
99532_at	0.00	0.00	0.00	0.00	-2.17	0.00	transducer of ErbB-2.1; Tob1	D78382
101446_at	0.00	0.00	0.00	0.00	-2.49	0.00	TPD52L1	AF004428
93266_at	0.00	-2.33	-1.90	0.00	-2.55	-2.51	tropomyosin 5; Tpm5	U04541
93509_at	0.00	0.00	-1.82	0.00	-2.58	-2.00	UBE2B	U57690
99507_at	0.00	0.00	-3.44	0.00	-2.86	-1.60	UCP	M21247
93392_at	-1.48	-1.66	0.00	0.00	-2.72	-1.67	UCP3	AB010742
95537_at	0.00	0.00	0.00	0.00	-2.26	0.00	ULK2	AB019577
92820_at	0.00	0.00	0.00	0.00	-2.43	-2.13	USP2	AI846522
92821_at	0.00	0.00	0.00	0.00	-2.73	-1.71	USP2	AF079565
114088_at	0.00	0.00	0.00	0.00	-2.55	-1.55	VAMP1	AI850070
92496_at	0.00	0.00	0.00	0.00	0.00	-2.59	VAMP5	AF035643
103001_at	0.00	-2.17	-1.96	0.00	-3.42	-2.12	vascular endothelial growth factor B; Vegfb	U43836
98549_at	0.00	-1.87	0.00	0.00	-2.11	0.00	vitronectin; Vtn	M77123
115141_at	0.00	0.00	-3.89	0.00	-5.60	0.00	UNK_AW049840	AW049840
103824_at	-1.39	-2.00	-2.01	0.00	-1.92	-1.71	WFS1	AF084482
103238_at	0.00	0.00	0.00	0.00	-4.41	0.00	wingless-related MMTV integration site 4; Wnt4	M89797
96063_at	0.00	0.00	0.00	0.00	-2.02	0.00	X-ray repair complementing defective repair in Chinese hamster cells 5; Xrcc5	X66323
99932_at	0.00	0.00	0.00	0.00	0.00	-6.45	ZFP100	U14556

101456_at	0.00	0.00	0.00	0.00	-2.16	-1.95	ZFP106	AF060245
108046_at	0.00	0.00	0.00	0.00	-2.37	-2.19	ZFP238	AI844802

Table 5. BMP-2-induced changes in the expression of known genes previously associated with bone or cartilage metabolism.

Gene Title	GenBank	Day 1	Day 2	Day 3	Day 4	Day 7	Day 14
Cell Surface Proteins							
OSTEOBLAST SPECIFIC FACT. 2	D13664	2.1+/- 0.2	4.1+/- 0.6	7.4+/- 0.2	11.6+/- 0.3	64.3+/- 6.7	42.7+/- 12
MEGAKAR. STIM. FACT.	AB034730	0+/- 0	5.6+/- 0.2	4.3+/- 0.2	4.8+/- 0.1	0+/- 0	0+/- 0
CADHERIN 11	D21253	0+/- 0	2.1+/- 0.3	2.9+/- 0	5.5+/- 3.3	37.9+/- 9.6	38.2+/- 7.3
CD44 ANTIGEN	M27129	0+/- 0	3.2+/- 0.5	3.9+/- 0.1	4.3+/- 0.3	4.5+/- 0.2	6+/- 0.6
CADHERIN 2	AB008811	0+/- 0	0+/- 0	0+/- 0	2.1+/- 0.5	15.9+/- 1.5	14.6+/- 0.2
SYNDECAN 2	U00674	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.1+/- 1.2	4.5+/- 0.2
INTEGRIN ALPHA V (CD51)	U14135	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.4+/- 1.4	5.7+/- 1
NEURAL CELL ADHESION MOLECULE	X07293	0+/- 0	0+/- 0	0+/- 0	4+/- 1.3	7.8+/- 1.9	3.4+/- 0.6
SYNDECAN 1	X15487	0+/- 0	2+/- 0.6	0+/- 0	0+/- 0	7.2+/- 1	6.9+/- 0.2
L-34 GALACTOSIDE-BINDING LECTIN.	X16074	0+/- 0	1.6+/- 0.3	2.1+/- 0.5	2.4+/- 0.5	6+/- 0.9	8.4+/- 0.9
GAP JUNC. MEMB. CHANN. PROT. ALPHA 1	X61576	0+/- 0	2.3+/- 0.5	0+/- 0	4+/- 0.8	8.4+/- 1.9	14.8+/- 3.6
INTEGRIN BETA 3 (CD61)	AF026509	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	7.2+/- 1
INTEGRIN BETA 2 (CD18)	X14951	2.6+/- 0.6	3+/- 0.3	2.8+/- 1.1	2.9+/- 0.3	2.9+/- 1.1	8.8+/- 0.1
VASCULAR CELL ADHESION MOLECULE 1	X67783	0+/- 0	2.2+/- 0	0+/- 0	2.9+/- 0.6	3.5+/- 0.9	6.8+/- 1.4
Cytokines							
FIBROBL. INDUCIB. SECRETED PROT.	M70642	5.1+/- 0.8	8+/- 1	10.2+/- 3.1	5.8+/- 1.7	19.1+/- 3.1	9.6+/- 0.5
STROMAL CELL DERIVED FACT. 5	D50462	2.2+/- 0.8	4.6+/- 0.5	8.3+/- 2.3	10.2+/- 3.4	17.5+/- 1.6	10.1+/- 1.1
MONO. CHEMOATTRAC. PROT.-2 PRECUR.	AB023418	0+/- 0	3.9+/- 1.8	6+/- 2.3	9+/- 2.3	9.4+/- 1.3	4.8+/- 2
SMALL INDUCIB. CYTOKINE A2	J04467	3.3+/- 0.6	7.4+/- 1.4	8.5+/- 1.9	8.4+/- 0.6	5.9+/- 0.9	1.9+/- 1
IL-1 BETA	M15131	1.1+/- 1.9	5.4+/- 2	4.4+/- 2.1	4.3+/- 1.1	0+/- 0	5.4+/- 0.9
CYSTEINE RICH PROT. 61	M32490	1.7+/- 0.5	2.6+/- 0.3	5.2+/- 0.3	7.8+/- 2.3	6.4+/- 1.8	2.8+/- 0.7
TGF, BETA 1	M13177	0+/- 0	2.6+/- 0.5	0+/- 0	2.9+/- 0.7	11.3+/- 0.8	7.6+/- 0.7
MIDKINE	M35833	0+/- 0	0+/- 0	0+/- 0	0+/- 0	22.2+/- 1.8	10.9+/- 1.5
INHIBIN BETA-A	X69619	0+/- 0	1.5+/- 0.4	2+/- 0.7	4.9+/- 4.4	5.2+/- 2.8	0+/- 0
WNT1 INDUCIB. SIG. PATHWAY PROT. 2	AF126063	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.3+/- 0.3
STROMAL CELL DERIVED FACT. 1	D43805	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	6.7+/- 1
COLONY STIM. FACT. 1 (MACROPHAGE)	M21149	2.8+/- 0.6	3+/- 1	1.9+/- 0.1	0+/- 0	3.1+/- 0.7	5.3+/- 0.7
PDGF, ALPHA	M29464	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.7+/- 1.4	0+/- 0
TGF, BETA 3	M32745	0+/- 0	0+/- 0	0+/- 0	2.6+/- 0.3	4.1+/- 1.3	1.9+/- 0.3
BONE MORPHOGENETIC PROT. 8A	M97017	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.6+/- 1.2
TPA REPRESSED GENE 1	S74318	-1.8+/- 0.1	0+/- 0	0+/- 0	0+/- 0	2.2+/- 0.2	9+/- 1.9
SECRETED FRIZZLED-RELATED PROT. 3	U91905	0+/- 0	0+/- 0	0+/- 0	0+/- 0	9.5+/- 1	2.2+/- 0.8
OSTEOPROTEGERIN	U94331	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.2+/- 0.6	0+/- 0
FOLLISTATIN	Z29532	0+/- 0	2.4+/- 0.3	0+/- 0	0+/- 0	4.2+/- 0.1	0+/- 0
GROWTH DIFFEREN. FACT. 1	M62301	0+/- 0	0+/- 0	0+/- 0	-4.7+/- 0	0+/- 0	0+/- 0
Extracellular Matrix Proteins							
TENASCIN C	X56304	0+/- 0	6.6+/- 1.6	14.4+/- 1.7	34.5+/- 13	91.6+/- 22.1	68.9+/- 7.6
SECRETED PHOSPHOPROT. 1	J04806	2.4+/- 0.9	3.4+/- 1.4	6+/- 1	15.7+/- 10.1	46.2+/- 8.7	98.3+/- 5.1
BIGLYCAN	X53928	1.8+/- 0.3	2.8+/- 0.5	4.2+/- 0.1	5.8+/- 1	11.6+/- 1.3	12.1+/- 1.4
PROCOLL., TYPE V, ALPHA 1	AB009993	0+/- 0	0+/- 0	3.1+/- 0.9	9+/- 2.2	17.1+/- 3.2	15.5+/- 1.5
CHONDROITIN SULFATE PROTEOGLYCAN 2	D16263	2.4+/- 1	3.1+/- 0.6	4.4+/- 0.5	5.4+/- 0.4	5.1+/- 1.2	2.4+/- 0.3
PROCOLL., TYPE V, ALPHA 2	L02918	0+/- 0	2.4+/- 0.3	3.6+/- 0.5	7+/- 0	17.2+/- 1	18.3+/- 0.4
AGGRECAN	L07049	0+/- 0	0+/- 0	0+/- 0	4.8+/- 2	27.6+/- 3.4	4.7+/- 0.8
FIBRONECTIN 1	M18194	0+/- 0	3.1+/- 0.2	3+/- 0.4	4.5+/- 0.4	7.8+/- 0.5	6.1+/- 0.4
ALPHA-1 TYPE-III COLLAGEN	M18933	0+/- 0	2.3+/- 0.3	2.2+/- 0.3	5+/- 0.2	13+/- 1.2	7.9+/- 0.7
THROMBOSPONDIN 1	M87276	3+/- 0.7	3.8+/- 0.8	3.9+/- 1.2	9.5+/- 3.4	27.2+/- 6.4	8.5+/- 2
PROCOLL., TYPE XII, ALPHA 1	U25652	0.5+/- 1.4	2+/- 0.3	3.9+/- 0.4	7.9+/- 2.5	29.4+/- 7.5	12.1+/- 1.3
PROCOLL., TYPE VI, ALPHA 2	X65582	0+/- 0	0+/- 0	0+/- 0	5.6+/- 0	14.1+/- 2.6	9.7+/- 0.5
COL8A1	X66977	0+/- 0	2.4+/- 0.2	1.8+/- 0.1	6.8+/- 1.4	23.4+/- 3.7	8.1+/- 3.1
LUMICAN	AF013262	0+/- 0	0+/- 0	0+/- 0	2.9+/- 0.5	8.5+/- 0.8	7.7+/- 1
COL11A2	AF100956	0+/- 0	0+/- 0	0+/- 0	0+/- 0	23.7+/- 0.2	24.2+/- 9
PROCOLL., TYPE XI, ALPHA 1	D38162	0+/- 0	0+/- 0	0+/- 0	0+/- 0	79.8+/- 1.6	49.7+/- 3.7
INTEGRIN BINDING SIALOPROT.	L20232	0+/- 0	0+/- 0	0+/- 0	0+/- 0	237.8+/- 9	174.1+/- 17.9
BONE GLA. PROT. 1	L24431	0+/- 0	0+/- 0	-4.1+/- 1	0+/- 0	14.9+/- 4.7	59.6+/- 3.8
PROCOLL., TYPE II, ALPHA 1	M65161	0+/- 0	0+/- 0	-1.8+/- 0.1	0+/- 0	168.1+/- 24	28.9+/- 3
PROCOLL., TYPE VI, ALPHA 1	Z18271	0+/- 0	0+/- 0	1.7+/- 0	3.4+/- 0.1	5+/- 0.3	4+/- 0.4
PROCOLL., TYPE X, ALPHA 1	Z21610	0+/- 0	0+/- 0	0+/- 0	0+/- 0	45.1+/- 29.8	5.6+/- 3.2
CARTILAGE OLIGOMERIC MATRIX PROT.	AF033530	0+/- 0	2.2+/- 0.4	0+/- 0	2.3+/- 0.6	10.8+/- 0.7	2.8+/- 0.4
CARTILAGE LINK PROT. 1	AF098460	0+/- 0	0+/- 0	0+/- 0	0+/- 0	14.9+/- 1.1	0+/- 0
PROCOLL., TYPE XIV, ALPHA 1	AJ131395	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.1+/- 0.8	2.1+/- 0.3
PROCOLL., TYPE IX, ALPHA 1	D17511	0+/- 0	0+/- 0	0+/- 0	0+/- 0	14+/- 0.7	0+/- 0
PROCOLL., TYPE XV	D17546	0+/- 0	0+/- 0	0+/- 0	0+/- 0	6.9+/- 0.6	3.9+/- 0.7
BONE GLA. PROT., RELATED SEQ. 1	L24430	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	77.8+/- 18.8

Gene Title	GenBank	Day 1	Day 2	Day 3	Day 4	Day 7	Day 14
EXTRACELLULAR MATRIX PROT. 1	L33416	0+/- 0	2.4+/- 0.2	2.6+/- 0.2	3+/- 0.4	3.2+/- 0.6	5.1+/- 0.2
ELASTIN	U08210	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.2+/- 1.8
ALPHA 3 TYPE IX COLLAGEN.	X91012	0+/- 0	0+/- 0	0+/- 0	0+/- 0	9.8+/- 0.8	0+/- 0
PROCOLL., TYPE IX, ALPHA 2	Z22923	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.4+/- 2.1	0+/- 0
Extracellular Proteins							
NEUROBLASTOMA, SUPP. OF TUMORIGEN. 1	D50263	0+/- 0	0+/- 0	0+/- 0	0+/- 0	6+/- 3.7	5.5+/- 1.1
IGF BINDING PROT. 4	X76066	0+/- 0	0+/- 0	0+/- 0	0+/- 0	7.1+/- 1.2	5.4+/- 0.4
APOLIPOPROT. E	D00466	0+/- 0	1.8+/- 0.4	2.4+/- 0.1	2.7+/- 0.1	3.8+/- 0.2	4.8+/- 0.3
IGF BINDING PROT. 3	X81581	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5+/- 0.4	3.2+/- 1
VITRONECTIN	M77123	-2.1+/- 0.2	-4.2+/- 1	-2.3+/- 0.3	0+/- 0	0+/- 0	0+/- 0
Intracellular Proteins							
CELL DIV. CYCLE 2 HOMOLOG A	M38724	1.6+/- 0.6	7.2+/- 1.1	10.6+/- 0.9	13.4+/- 3.9	12.1+/- 1.6	4+/- 0.2
LYSYL OXIDASE	M65142	0+/- 0	5.3+/- 0.7	8.9+/- 1	12.6+/- 0.6	22.8+/- 1.3	15.5+/- 0.9
PROCOLL-LYS., 2-OXOGLUT.5-DIOXYGEN. 2	AF080572	0+/- 0	2.9+/- 0.4	6.2+/- 2.6	15.2+/- 4.4	13.5+/- 1.8	11.6+/- 1.7
ALK. PHOSPHATASE 2, LIVER	J02980	0+/- 0	0+/- 0	5+/- 1	6.1+/- 3.6	32.6+/- 2.9	18.5+/- 3.8
HEME OXYGENASE (DECYCLING) 1	X13356	1.9+/- 0.3	4+/- 1.5	4.5+/- 1.2	7.3+/- 2.3	8.2+/- 0.3	7.6+/- 1
PROCOLL-LYS., 2-OXOGLUT. 5-DIOXYGEN. 3	AF046783	0+/- 0	3.7+/- 0.6	4.6+/- 0.2	5.1+/- 0.5	8.5+/- 0.7	3.8+/- 0.9
PHOSPHOLIPASE A2, GROUP 4	M72394	0+/- 0	2.6+/- 0.5	3.9+/- 0.1	6.9+/- 1.8	7.2+/- 0.6	4.4+/- 0.1
ATPASE, H+ TRANSPORTING, LYSOSOMAL I	AB022322	0+/- 0	0+/- 0	3.1+/- 0.8	0+/- 0	7+/- 1.4	27.8+/- 2.4
LYSYL OXIDASE-LIKE PROT. 2	AF117951	0+/- 0	0+/- 0	0+/- 0	7.2+/- 0.6	7.7+/- 0.8	2.1+/- 0.4
PROSTAGLAN.-ENDOPEROX. SYNTHASE 2	M64291	0+/- 0	2.5+/- 0.3	2.3+/- 0	8.9+/- 3.4	5.5+/- 1.2	-0.3+/- 1.6
CREATINE KINASE, BRAIN	M74149	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.6+/- 0.6	28.6+/- 2
CALRETICULIN	X14926	0+/- 0	2.9+/- 0.2	3+/- 0.3	4.1+/- 0.6	5.5+/- 0.2	3.9+/- 0.3
BCL2-ASSOCIATED X PROT.	L22472	0+/- 0	2.5+/- 0.4	2.1+/- 0.2	0+/- 0	4.9+/- 0.8	0+/- 0
CARBONIC ANHYDRASE 2	M81022	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0.3+/- 1.4	13.8+/- 3.7
LYSYL OXIDASE-LIKE	U79144	0+/- 0	2+/- 0.1	0+/- 0	3.5+/- 0.1	4.6+/- 0.6	3.4+/- 0.3
FATTY ACID SYNTHASE	X13135	0+/- 0	-1.5+/- 2.6	-4.4+/- 0.6	-3.3+/- 2.4	-3.9+/- 1.2	-0.2+/- 2.3
Proteases							
TISSUE INHIB. OF METALLOPROT.	M17243	1.1+/- 2	12.8+/- 3.2	25.4+/- 7.6	48.1+/- 11.(	100.3+/- 11	56+/- 3.5
SERINE PROTEASE INHIB. 2-2	M64086	0+/- 0	6.8+/- 1.2	7.4+/- 0.8	8.3+/- 2.5	7.7+/- 1.3	2.4+/- 1.1
BONE MORPHOGENETIC PROT. 1	L24755	0+/- 0	0+/- 0	2.9+/- 0.5	6.8+/- 1.7	23+/- 4.1	18.1+/- 0.3
MATRIX METALLOPROT. 14	U54984	0+/- 0	2.8+/- 0.4	2.7+/- 0	7+/- 1.3	23.1+/- 3.8	18.1+/- 4.6
CATHEPSIN K	X94444	0+/- 0	0+/- 0	0+/- 0	6.1+/- 4	11.3+/- 3.1	47+/- 1.6
MATRIX METALLOPROT. 9	Z27231	0+/- 0	0+/- 0	0+/- 0	20+/- 16.8	16.3+/- 12.:	221.5+/- 18.5
PROCOLL. C-PROT. ENHANCER PROT.	AB008548	0+/- 0	0+/- 0	0+/- 0	3.3+/- 0.5	7+/- 1.2	6.7+/- 0.8
PLASMINOGEN ACT., TISSUE	J03520	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.3+/- 1.3	4.6+/- 0.6
MATRIX METALLOPROT. 2	M84324	-2.1+/- 0.3	-1.8+/- 0.1	0.1+/- 1.7	2.7+/- 0.4	8.1+/- 1.1	7.2+/- 0.6
UROKINASE PLASMINOGEN ACT. RECEPT.	X62700	1.7+/- 0.3	3.1+/- 0.5	0+/- 0	4.4+/- 1	7.8+/- 0.7	2.3+/- 0.4
MATRIX METALLOPROT. 13	X66473	0+/- 0	0+/- 0	0+/- 0	0+/- 0	19.3+/- 2.5	144.8+/- 24.1
PLASMINOGEN ACT. INHIB., TYPE I	M33960	0+/- 0	2.9+/- 0.7	2.8+/- 0.3	5+/- 1.3	3.2+/- 0.5	0+/- 0
TISSUE INHIB. OF METALLOPROT. 2	X62622	0+/- 0	1.7+/- 0.1	1.8+/- 0	2.6+/- 0.4	4.7+/- 0.9	3.8+/- 0.5
Receptors							
TGF BETA INDUCED, 68 KDA	L19932	2.8+/- 0.7	6+/- 2	5.6+/- 0.7	7.8+/- 0.7	5.3+/- 1	2+/- 0.4
PARATHYROID HORMONE RECEPT.	X78936	0+/- 0	0+/- 0	3+/- 0.1	6+/- 1.9	57.4+/- 1.3	25.5+/- 1.1
PTP, RECEPT. TYPE, D	D13903	0+/- 0	0+/- 0	0+/- 0	1.6+/- 0.1	6.6+/- 0.4	8.7+/- 2.2
IL-4 RECEPT., ALPHA	M29854	0+/- 0	4.8+/- 1.4	2.9+/- 0.1	0+/- 0	8.1+/- 0.7	0+/- 0
FIBROBL. GROWTH FACT. RECEPT. 2	M86441	0+/- 0	0+/- 0	0+/- 0	0+/- 0	15.3+/- 2.5	7.9+/- 1.3
COLONY STIM. FACT. 1 RECEPT.	X68932	1.8+/- 0.5	3.2+/- 0.4	3.3+/- 0.5	4.1+/- 0.6	3.5+/- 0.6	10.9+/- 0.9
ACTIVIN A RECEPT., TYPE 1	L15436	0+/- 0	0+/- 0	1.9+/- 0.2	2.7+/- 0.3	4.6+/- 0.1	0+/- 0
COLONY STIM. FACT. 3 RECEPT.	M58288	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.9+/- 0.9
COLONY STIM. FACT. 2 RECEPT., ALPHA	M85078	0+/- 0	2.6+/- 0.7	3.3+/- 0.3	0+/- 0	4.8+/- 0.8	3.9+/- 0.4
TGF BETA RECEPT. II	S69114	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.7+/- 1
Signal Transduction							
C-SRC TYROSINE KINASE	U05247	0+/- 0	2.6+/- 0.3	0+/- 0	2.9+/- 0.1	4.9+/- 0.4	3.6+/- 0.2
Transcription Factors							
MAD HOMOLOG 6	AF010133	6.7+/- 3	8.1+/- 1.7	9.9+/- 2.3	4.6+/- 0.9	7.7+/- 2.9	5.5+/- 0.5
INHIB. OF DNA BINDING 1	M31885	3.6+/- 0.7	8.1+/- 1.9	7.6+/- 0.8	4.9+/- 1.9	4.4+/- 1.7	4.9+/- 0.6
INHIB. OF DNA BINDING 2	M69293	2.4+/- 0.6	4.5+/- 0.6	5.7+/- 1.4	4.8+/- 0.5	11.9+/- 3.2	5.7+/- 0.7
RUNT RELATED TRANSCRIP. FACT. 2	D14636	0+/- 0	2.6+/- 0.5	3.8+/- 0.2	8.9+/- 2.7	15.8+/- 1.3	20.1+/- 4.9
JUN-B ONCOGENE	J03236	0.9+/- 1.7	4.4+/- 0.5	2.7+/- 0	3.6+/- 1.2	5.1+/- 1	2.3+/- 0.4
SCLERAXIS	S78079	0+/- 0	3.8+/- 1.9	6.9+/- 3.8	0+/- 0	19.4+/- 6	0+/- 0
SIG. TRANS. AND ACT. OF TRANSCRIP. 1	U06924	0+/- 0	2.2+/- 0.3	3.5+/- 0.9	4.7+/- 0.3	2.7+/- 0.1	5.2+/- 3.2
DISTAL-LESS HOMEOBOX 5	U67840	0+/- 0	0+/- 0	0+/- 0	0+/- 0	8.5+/- 1	7.5+/- 1

Gene Title	GenBank	Day 1	Day 2	Day 3	Day 4	Day 7	Day 14
NUC. FACT. ACTIV. T-CELLS, CYTOPLAS. 1	AF049606	0+/- 0	0+/- 0	0+/- 0	0+/- 0	2.7+/- 0.8	5.2+/- 0.8
MAD HOMOLOG 2	U60530	0+/- 0	2+/- 0.3	2.5+/- 0.2	0+/- 0	4.5+/- 0.7	0+/- 0
SLUG	U79550	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.4+/- 3.1	0+/- 0
INHIB. OF DNA BINDING 4	X75018	2.8+/- 1.4	3.5+/- 0.6	3.7+/- 1.2	0+/- 0	1.7+/- 0.2	6+/- 0.3

Table 6. BMP-2-induced changes in the expression of known genes not explicitly associated with bone or cartilage metabolism*.

Gene Title	GenBank	Day 1	Day 2	Day 3	Day 4	Day 7	Day 14
Cell Surface Proteins							
CD68 ANTIGEN	X68273	2.2+/- 0.5	3.2+/- 0.5	3.8+/- 0.6	5.1+/- 0.6	6.5+/- 1.1	15.8+/- 0.5
FIBROBL. ACTIVATION PROT.	Y10007	0+/- 0	0+/- 0	0+/- 0	2.3+/- 0.1	5.6+/- 0.7	10.9+/- 0.4
CD9 ANTIGEN	L08115	0+/- 0	0+/- 0	0+/- 0	0+/- 0	3.5+/- 0.3	4.1+/- 0.1
HEPATIC LIPASE	X58426	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.5+/- 0.9
SELECTIN, PLATELET (P-SELECTIN) LIGAND	X91144	0+/- 0	2.3+/- 0.2	2.5+/- 0.3	3.2+/- 0.4	3.2+/- 0.3	7.2+/- 0.6
EPHRIN B1	Z48781	0+/- 0	0+/- 0	1.6+/- 0.1	0+/- 0	5.9+/- 1	3.4+/- 1.2
Cytokines							
MONO. CHEMOTACTIC PROT.-3	S71251	4.1+/- 0.7	9.3+/- 1.7	5.7+/- 2.3	8.1+/- 2.2	6.6+/- 1.5	0+/- 0
SMALL INDUCIB. CYTOKINE A12	U50712	1.9+/- 0.1	4.1+/- 2.1	5.6+/- 0.8	3.8+/- 0.1	10.7+/- 2	0+/- 0
SECRETED FRIZZLED-RELATED PROT. 1	U88566	0+/- 0	2.8+/- 0.9	5.9+/- 0.5	11.4+/- 5.9	9.3+/- 1.8	2.5+/- 0.5
SMALL INDUCIB. CYTOKINE B MEMBER 9	M34815	0+/- 0	0+/- 0	3.4+/- 0.5	5.2+/- 0.4	3.6+/- 0.6	7+/- 7.7
VASCULAR ENDOTHELIAL GROWTH FACT. B	U48800	0+/- 0	-2.3+/- 1	0+/- 0	-9.6+/- 9.3	-7.8+/- 3.9	-2.7+/- 0.4
SMALL INDUCIB. CYTOKINE A11	U40672	-4.1+/- 2	-3.4+/- 0.4	0+/- 0	-1.5+/- 0.3	-2.6+/- 1	-2.4+/- 0.5
Extracellular Proteins							
LIPOCORTIN 1	M24554	2+/- 0.5	2.4+/- 0.2	2.7+/- 0.6	3.8+/- 0.6	4.5+/- 0.8	5+/- 0.2
SECRETED FRIZZLED-RELATED PROT. 4	AF117709	0+/- 0	-1.3+/- 0.1	0+/- 0	0+/- 0	0+/- 0	12.7+/- 0.8
SUPEROX. DISMUTASE 3, EXTRACELL.	D50856	0+/- 0	4+/- 1.1	3.8+/- 0.1	3.6+/- 1	4.4+/- 0.8	0+/- 0
ANNEXIN A4	U72941	0+/- 0	1+/- 1.8	2.1+/- 0.2	2.9+/- 0.4	3.8+/- 0.9	4.2+/- 0.1
AMYLOID BETA (A4) PRECUR. PROT.	U84012	0+/- 0	1.8+/- 0.2	1.6+/- 0.2	2.5+/- 0	4+/- 0.6	2.7+/- 0.4
Intracellular Proteins							
PLASTIN 2, L	D37837	0+/- 0	4.5+/- 0.8	4.3+/- 0.4	5.2+/- 0.3	8.1+/- 0.9	11.4+/- 1.1
CYSTEINE-RICH PROT. 2	AF037208	0+/- 0	3.8+/- 0.3	8.4+/- 1.9	15.8+/- 3.4	25.8+/- 7.5	6.5+/- 0.8
FGF REGULATED PROT.	U04204	0+/- 0	3.7+/- 0.7	4+/- 0.9	5.7+/- 1.4	5.6+/- 0.7	5.9+/- 0.8
CARBONYL REDUCTASE 2	D26123	1.6+/- 0.4	4.6+/- 0.4	6.8+/- 0.5	5.1+/- 0.2	2.1+/- 0.1	1.9+/- 0.2
ENDOPLASMIC RETICULUM PROT.	M73329	0+/- 0	2.8+/- 0.2	2.8+/- 0.3	4.8+/- 0.8	7+/- 1.6	4.3+/- 0.3
CYCLIN D1	S78355	0+/- 0	3.2+/- 0.1	4.5+/- 0.2	0+/- 0	7.2+/- 0.6	6.4+/- 0.6
TRANSPORTER 1, ATP BINDING CASSETTE	U60019	0+/- 0	1.8+/- 0.4	4.2+/- 0.2	3.7+/- 0.9	4.9+/- 0.2	5.3+/- 2.9
2'-5' OLIGOADENYLATE SYNTHETASE 1A	X04958	1.8+/- 0.2	2.8+/- 0.6	4.3+/- 0.7	5.8+/- 1.2	5.1+/- 0.4	3.7+/- 0.5
CALCIUM BIND. PROT. A11 (CALGIZZARIN)	M16465	1.9+/- 0.5	2.5+/- 0.1	2.8+/- 0.5	3.4+/- 0.2	4.4+/- 0.7	4.2+/- 0.3
MYOSIN LIGHT CHAIN, ALKALI, ATRIA	M19436	0+/- 0	0+/- 0	0+/- 0	0+/- 0	8+/- 2.5	5.5+/- 1.1
RETINOL BINDING PROT. 1, CELLULAR	X60367	0+/- 0	0+/- 0	0+/- 0	4.1+/- 0.9	7.1+/- 0.8	2.4+/- 0.1
CYCLIN A2	Z26580	0+/- 0	3.1+/- 0.5	3.6+/- 0.7	4.8+/- 0.3	5.7+/- 0.3	1.9+/- 0.2
PROCOLL-LYS., 2-OXOGLUT. 5-DIOXYGEN. 1	AF046782	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.2+/- 1.1	3.4+/- 0.4
GALACTOSYLTRANSFERASE, POLYPEP. 1	J03880	0+/- 0	0+/- 0	0+/- 0	0+/- 0	8+/- 1.8	0+/- 0
RHO, GDP DISSOCIATION INHIB. BETA	L07918	0+/- 0	4+/- 0.4	3.1+/- 0.3	3.3+/- 0.5	4.4+/- 0.3	3.8+/- 1.2
STEROL O-ACYLTRANSFERASE 1	L42293	0+/- 0	2.5+/- 0.6	2.2+/- 0.2	3.6+/- 0.2	5.4+/- 0.9	2.9+/- 0.7
CYCLIN D2	M83749	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.2+/- 0.1	3.7+/- 0.1
RAT PROTEASOME HOMOLOG	S59862	0+/- 0	2.8+/- 0.5	3.3+/- 0.4	5.5+/- 0.9	0+/- 0	3.8+/- 4.1
LYMPHOCYTE CYTOSOLIC PROT. 2	U20159	0+/- 0	2.4+/- 0.4	2.5+/- 0.3	3.1+/- 0.7	3.2+/- 0.6	4.8+/- 0.2
TRANSPORTER 2, ATP BINDING CASSETTE	U60087	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.7+/- 2.1
CAPPING PROT., GELSOLIN-LIKE	X54511	0+/- 0	2.6+/- 0.2	2.6+/- 0.4	3+/- 0.1	3.8+/- 0.4	4.7+/- 1
CYCLIN B1, RELATED SEQ. 1	X58708	0+/- 0	2.4+/- 0.2	3.1+/- 0.2	3.9+/- 0.4	4.1+/- 0.1	1.7+/- 0.2
CYCLIN B2	X66032	0+/- 0	3.6+/- 0.5	2.7+/- 0.6	4.4+/- 0.7	2.9+/- 0.2	2.2+/- 0.4
HISTONE DEACETYLASE 1	X98207	0+/- 0	0+/- 0	3.2+/- 0.2	0+/- 0	7.3+/- 0.7	3.2+/- 0.3
Proteases							
MATRIX METALLOPROT. 23	AF085742	0+/- 0	0+/- 0	0+/- 0	11.2+/- 1	39.9+/- 3	15.7+/- 0.6
CASPASE 6	Y13087	0+/- 0	0+/- 0	2.8+/- 1.3	4.9+/- 2.1	7.6+/- 1.6	7.7+/- 0.9
CATHEPSIN H	U06119	0+/- 0	2.1+/- 0.4	2.3+/- 0.2	3.6+/- 0.2	5.8+/- 0.8	4.4+/- 0.6
CATHEPSIN S	AF038546	1.8+/- 0.3	2.8+/- 0.5	3.2+/- 0.4	4+/- 0	3.8+/- 0.5	5.4+/- 1
PROTEOSOME SUBUNIT, BETA TYPE 8	U22032	0+/- 0	2.9+/- 0.4	3.5+/- 0.2	3.7+/- 0.6	3.4+/- 0.3	6.3+/- 4.3
SERINE PROTEASE INHIB. 4	X70296	0+/- 0	0+/- 0	0+/- 0	0+/- 0	3.4+/- 0.3	8.9+/- 1.2
Receptors							
IL-2 RECEPT., GAMMA CHAIN	L20048	0+/- 0	3.9+/- 0.7	4.7+/- 0.2	5.6+/- 0.5	7.9+/- 0.8	5.3+/- 0.9
CYTOKINE RECEPT.-LIKE FACT. 1	AB040038	3+/- 1.1	7.6+/- 1	7.2+/- 2.9	14.7+/- 6.4	8.8+/- 4	2.1+/- 0.5
FC RECEPT., IGG, HIGH AFFINITY I	X70980	2.7+/- 0.5	7.6+/- 2.7	7.3+/- 0.6	6.7+/- 1.2	4.8+/- 1.1	0+/- 0
PTP, RECEPT. TYPE, C	M14342	2.5+/- 0.5	3.4+/- 0.4	4.3+/- 1.7	5.2+/- 0.9	3.3+/- 0.8	6.8+/- 0.8
CHEMOKINE (C-C) RECEPT. 2	U51717	2.9+/- 1	6.1+/- 0.8	5.1+/- 1.3	4.2+/- 0.4	3.4+/- 0.6	3.6+/- 0.4
TNF RECEPT. SUPERFAMILY, MEMBER 1A	L26349	1.4+/- 0.3	2.7+/- 0.2	1.9+/- 0	2.8+/- 0.1	4.1+/- 0.2	4+/- 0.1
CHEMOKINE (C-C) RECEPT. 1	U29678	3.4+/- 1.6	4.9+/- 1	2.4+/- 0.7	2.8+/- 0.2	1.9+/- 0.2	13.3+/- 0.6
PDGF RECEPT., BETA POLYPEPTIDE	X04367	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.6+/- 1.5	4.8+/- 1

Gene Title	GenBank	Day 1	Day 2	Day 3	Day 4	Day 7	Day 14
PTP, RECEPT. TYPE, S	X82288	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.1+/- 0.7	5.4+/- 0.5
FRIZZLED-1	AF054623	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5+/- 1	1.4+/- 0.4
ANGIOTENSIN RECEPT.-LIKE 1	AJ007612	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.2+/- 0.6	2.9+/- 0.1
LEUKEMIA INHIB.Y FACT. RECEPT.	D17444	0+/- 0	1.2+/- 0.1	0+/- 0	0+/- 0	3.2+/- 0.3	9.9+/- 1.3
FC RECEPT., IGG, LOW AFFINITY III	M14215	0+/- 0	3.6+/- 0.4	3.4+/- 0.3	3.6+/- 0	4.2+/- 0.4	0+/- 0
PTP, RECEPT. TYPE, A	M36033	0+/- 0	0+/- 0	0+/- 0	2.9+/- 0.1	3.9+/- 0.7	4+/- 0.4
CHEMOKINE (C-C) RECEPT. 5	U47036	2.7+/- 1	4.8+/- 1.9	2.6+/- 0.1	3.5+/- 0.2	3.2+/- 0.2	1.5+/- 0.2
EPH RECEPT. A2	X76010	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.1+/- 0.9	3+/- 0.2
EPH RECEPT. B3	Z49086	0+/- 0	0+/- 0	0+/- 0	2.5+/- 1	7.1+/- 1.5	2.9+/- 0.2
RETINOID X RECEPT. GAMMA	X66225	0+/- 0	0+/- 0	0+/- 0	-4.2+/- 3.1	-4.5+/- 0.4	-4.6+/- 2.5
Signal Transduction							
APLYSIA RAS-RELATED HOMOLOG 9	X80638	0+/- 0	0+/- 0	3.5+/- 0.4	5.7+/- 0.3	7+/- 0.8	7.6+/- 0.2
FYN PROTO-ONCOGENE	M27266	0+/- 0	0+/- 0	1.5+/- 0.4	2.2+/- 0.1	4.2+/- 0.5	4.4+/- 0.7
RAS P21 PROT. ACT. 3	U20238	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.4+/- 0.4	4.7+/- 0.5
DOWNSTREAM OF TYROSINE KINASE 1	U78818	0+/- 0	1.7+/- 0.5	2.7+/- 1.1	4.5+/- 1.4	5.4+/- 1.5	3.3+/- 0.1
MITOGEN-ACTIVATED PROT. (KINASE)4	U88984	0+/- 0	2+/- 0.3	2.6+/- 0.3	3.1+/- 0.1	5.2+/- 0.5	4.9+/- 0.7
VAV ONCOGENE	X64361	0+/- 0	4.3+/- 0.4	3.2+/- 0.2	4+/- 0.4	2.3+/- 0.2	0+/- 0
HEMATO. CELL SPECIFIC LYN SUBSTR. 1	X84797	2.7+/- 1.3	5.6+/- 1.5	4.2+/- 1.3	3.2+/- 0.6	4+/- 0.9	3.1+/- 0.5
REGULATOR OF G-PROT. SIG. 2	AF215668	0+/- 0	1.5+/- 0.4	2.9+/- 0.9	3.2+/- 0.2	2.8+/- 0.6	5.6+/- 0.7
ANNEXIN A8	AJ002390	0+/- 0	0+/- 0	0+/- 0	0+/- 0	8.3+/- 1.6	3.8+/- 0.2
CYCLIN-DEPENDENT KINASE 4	L01640	0+/- 0	2.4+/- 0.2	2.5+/- 0	3.4+/- 0.7	5.2+/- 0.7	3.5+/- 0.1
INOSITOL POLYPHOS.-5-PHOSPHATASE	U52044	0+/- 0	1.9+/- 0.3	1.9+/- 0.5	0+/- 0	3.7+/- 0.8	4.3+/- 0.4
CYTO. INDUCIB. SH2-CONTAINING PROT. 3	U88328	0+/- 0	3.6+/- 0.7	0+/- 0	0+/- 0	5.6+/- 1.5	1.8+/- 0.2
FELINE SARCOMA ONCOGENE	X12616	0+/- 0	0+/- 0	0+/- 0	0+/- 0	7+/- 1	0+/- 0
PTP, NON-RECEPT. TYPE 12	X86781	0+/- 0	0+/- 0	0+/- 0	0+/- 0	3.2+/- 1.1	4.9+/- 0.5
APLYSIA RAS-RELATED HOMOLOG B	X99963	0+/- 0	0+/- 0	0+/- 0	0+/- 0	3.5+/- 0.5	4+/- 0.4
Structural Proteins							
TROPONIN T2, CARDIAC	L47570	0+/- 0	0+/- 0	-1.3+/- 0.1	4+/- 2.7	12.4+/- 5.2	3.4+/- 1.6
NESTIN	AF076623	0+/- 0	0+/- 0	0+/- 0	0+/- 0	6.1+/- 1.2	0+/- 0
CORONIN, ACTIN BINDING PROT. 1A	AF143955	1.8+/- 0.4	4.1+/- 0.8	2.9+/- 0	3.3+/- 0.4	3.3+/- 0.1	3.7+/- 1.1
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE	M76601	0+/- 0	-3.9+/- 3.9	0+/- 0	-9.1+/- 9.4	-8.9+/- 6.3	-6.6+/- 6
Transcription Factors							
MYOGENIN	D90156	0+/- 0	6.9+/- 5.1	6.6+/- 2.8	17.2+/- 13.(	15.8+/- 10.(	0+/- 0
MYOGENIC DIFFEREN. 1	M84918	6.4+/- 0.9	7.5+/- 3.1	5.3+/- 3.6	0+/- 0	8+/- 3.7	0+/- 0
SFFV PROVIRAL INTEGRATION 1	X17463	0+/- 0	2.1+/- 0.6	4.2+/- 0	2.8+/- 0.3	4.4+/- 1	8+/- 1
ELK3, ETS ONCOGENE FAMILY	Z32815	0+/- 0	2.4+/- 0.3	2.7+/- 0.5	0+/- 0	6.4+/- 0.5	4.6+/- 0.5
INS-1 WINGED HELIX	U83112	1.6+/- 0.5	2.6+/- 0.5	0+/- 0	2.4+/- 0.4	3.1+/- 0.3	4.4+/- 1.8
INTERFERON REG. FACT. 1	M21065	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	5.4+/- 2.4
T-CELL ACUTE LYMPHOCYTIC LEUKEMIA 1	U01530	4.1+/- 1.7	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0
PEROX. PROLIF. ACTIV. RECEPT. GAMMA	U09138	0+/- 0	0+/- 0	3.3+/- 0.4	0+/- 0	0+/- 0	4.9+/- 0.4
NFKB INHIB., ALPHA	U36277	0+/- 0	0+/- 0	0+/- 0	0+/- 0	0+/- 0	4.3+/- 0.4

* Genes were assigned to this table after three searches of the PubMed database. The first search looked for papers in which the gene name OR an MGI alias were used in the tile. The second search looked for all papers in which the following terms were used in the tile: cartilage OR bone OR chondrogenesis OR osteogenesis OR BMP OR endochondral OR fracture OR osteoblast OR osteoclast. The third search looked for the intersection of searches 1 AND 2. If no records were returned in the third search, then it was determined that there is no explicit association between the gene and bone or cartilage metabolism.

Table 5. Summary of cells stained with an antisense probe for MMP23 mRNA*

		Day					
Treatment	MMP23 mRNA Positive Cell	1	2	3	4	7	14
BUFFER	Fibroblast	–	–	–	–	–	–
	Macrophage	–	–	–	–	–	–
	Chondrocyte-like	N/A	N/A	N/A	N/A	N/A	N/A
	Chondrocyte	N/A	N/A	N/A	N/A	N/A	N/A
	Marrow cell	N/A	N/A	N/A	N/A	N/A	N/A
	Osteoblast/Osteocyte	N/A	N/A	N/A	N/A	N/A	N/A
HBMP-2	Fibroblast	+	-	-	-	-	-
	Macrophage	+	-	-	-	-	-
	Chondrocyte-like	N/A	N/A	N/A	+	N/A	N/A
	Chondrocyte	N/A	N/A	N/A	N/A	+	N/A
	Marrow cell	N/A	N/A	N/A	N/A	N/A	-
	Osteoblast/Osteocyte	N/A	N/A	N/A	N/A	N/A	+

* Binding of sense probe was not detected in either treatment group.

N/A: Cell type not present in section.
+: Slight staining intensity
++: Mild staining intensity
-: Staining not detected

Accordingly, the results show for the first time that CLF-1 and MMP23 are expressed in cells associated with bone and cartilage. These genes will thus be useful targets in diagnostics and in drug design for diseases relating to bone and cartilage formation.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

Claims:

1. A computer-readable medium comprising a plurality of digitally encoded values representing the levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 during bone or cartilage formation.

2. The computer-readable medium of claim 1, comprising values representing levels of expression of at least 5 genes listed in Table 1, 2, 5 and/or 6 during bone or cartilage formation.

3. The computer-readable medium of claim 1, comprising values representing levels of expression of CLF-1 and MMP23 during bone or cartilage formation.

4. The computer-readable medium of claim 1, comprising values representing levels of expression of a plurality of genes listed in Table 6.

5. The computer-readable medium of claim 1, further comprising at least one value representing a level of expression of at least one gene that is up-or down-regulated during bone or cartilage formation in a precursor cell.

6. The computer-readable medium of claim 1, wherein the values represent ratios of, or differences between, a level of expression of a gene in one sample and the level of expression of the gene in another sample.

7. The computer-readable medium of claim 1, wherein less than about 50% of the values represent expression levels of genes which are not listed in Table 1, 2, 5 and/or 6.

8. A computer system, comprising:
a database comprising values representing expression levels of a plurality of genes listed in Table 1, 2, 5 and/or 6 during bone or cartilage formation; and,
a processor having instructions to,
receive at least one query value representing at least one level of expression of at least one gene listed in Table 1, 2, 5 and/or 6; and,
compare the at least one query value and the at least one database value.

9. The computer system of claim 8, wherein the query value represents the level of expression of a gene listed in Table 1, 2, 5 and/or 6 in a diseased cell of a subject having or susceptible of having a disease selected from the group consisting of osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; periondontal disease; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss caused by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone fractures.

10. A computer program for analyzing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a cell, the computer program being disposed on a computer readable medium and including instructions for causing a processor to:
receive query values representing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a query cell, and,
compare the query values with levels of expression of the plurality of genes listed in Table 1, 2, 5 and/or 6 in a reference cell.

11. A composition comprising a plurality of detection agents of genes listed in Table 1, 2, 5 and/or 6, which detection agents are capable of detecting the expression of the genes or the polypeptides encoded by the genes, and wherein less than about 50% of the detection agents are of genes which are not listed in Table 1, 2, 5 and/or 6.

12. The composition of claim 11, comprising detection agents of CLF-1 or MMP23.

13. The composition of claim 11, wherein the detection agents are isolated nucleic acids that hybridize specifically to nucleic acids corresponding to the genes.

14. The composition of claim 12, comprising isolated nucleic acids that hybridize specifically to at least five genes of Table 6.

15. The composition of claim 11, comprising isolated nucleic acids that hybridize specifically to at least 10 different genes listed in Table 1, 2, 5 and/or 6.

16. The composition of claim 15, comprising isolated nucleic acids that hybridize specifically to at least 100 different genes listed in Table 1, 2, 5 and/or 6.

17. A solid surface to which are linked a plurality of detection agents of genes which are listed in Table 1, 2, 5 and/or 6, which detection agents are capable of detecting the expression of the genes or the polypeptides encoded by the genes, and wherein less than about 50% of the detection agents are not detecting genes listed in Table 1, 2, 5 and/or 6.

18. The solid surface of claim 17, wherein the detection agents are isolated nucleic acids that hybridize specifically to the genes.

19. The solid surface of claim 18, wherein the detection agents are covalently linked to the solid surface.

20. A composition comprising a plurality of antagonists of a plurality of genes listed in Table 1, 2, 5 and/or 6.

21. The composition of claim 20, wherein the antagonists are antisense nucleic acids, siRNAs, ribozymes or dominant negative mutants.

22. A composition comprising a plurality of agonists of a plurality of genes listed in Table 1, 2, 5 and/or 6.

23. A method for determining the difference between levels of expression of a plurality of genes in Table 1, 2, 5 and/or 6 in a cell and reference levels of expression of the genes, comprising

providing RNA from the cell;

determining levels of RNA of a plurality of genes listed in Table 1, 2, 5 and/or 6 to obtain the levels of expression of the plurality of genes in the cell; and

comparing the levels of expression of the plurality of genes in the cell to a set of reference levels of expression of the genes,

to thereby determine the difference between levels of expression of the plurality of genes listed in Table 1, 2, 5 and/or 6 in the cell and reference levels of expression of the genes.

24. The method of claim 23, wherein the set of reference levels of expression includes the levels of expression of the genes during bone or cartilage formation.

25. The method of claim 21, wherein the set of reference levels of expression further includes the levels of expression of the genes in a precursor cell.

26. The method of claim 25, wherein the cell is a cell of a subject having or susceptible of having a disease selected from the group consisting of osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteoma and osteoblastoma; periondontal disease; hyperparathyroidism; hypercalcemia of malignancy; Paget's disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss caused by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone fractures.

27. The method of claim 23, comprising incubating a nucleic acid sample derived from the RNA of the cell of the subject with nucleic acids corresponding to the genes, under conditions wherein two complementary nucleic acids hybridize to each other.

28. The method of claim 27, wherein the nucleic acids corresponding to the genes are attached to a solid surface.

29. The method of claim 23, comprising entering the levels of expression of the plurality of genes into a computer which comprises a memory with values representing the set of reference levels of expression.

30. The method of claim 29, wherein comparing the level comprises providing to the computer instructions to perform.

31. A method for determining whether a subject has or is likely to develop a disease related to bone or cartilage resorption, comprising obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant differences in the levels of expression of the plurality of genes indicates that the subject has or is likely to develop a disease related to bone or cartilage resorption.

32. The method of claim 31, wherein the disease is selected from the group consisting of osteoporosis, osteopenia, periondontal disease; osteolytic lesions produced by bone metastasis; bone loss due to immobilization or sex hormone deficiency; bone and cartilage loss caused by an inflammatory disease, rheumatoid arthritis and osteoarthritis.

33. A method for determining whether a subject has or is likely to develop a disease related to bone or cartilage formation, comprising obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant similarities in the levels of expression of the plurality of genes indicates that the subject has or is likely to develop a disease related to bone or cartilage formation.

34. The method of claim 33, wherein the disease is selected from the group consisting of osteodystrophy, osteohypertrophy, osteoblastoma, osteopertrusis, osteogenesis imperfecta, osteoma and osteoblastoma, hyperparathyroidism; hypercalcemia of malignancy; and Paget's disease.

35. A method for determining the effectiveness of a treatment intended to stimulate bone or cartilage formation, comprising obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant similarities in the levels of expression of the plurality of genes indicates that the treatment is effective.

36 The method of claim 35, wherein the biological sample is obtained from the healing region of a bone fracture and a similarity in levels of expression of the plurality of genes in the cell of the subject and the reference levels of expression indicates that the fracture is healing.

37. The method of claim 35, further comprising iteratively providing a biological sample from the subject, such as to determine an evolution of the levels of expression of the genes in the subject.

38. The method of claim 35, wherein the set of reference levels of expression is in the form of a database.

39. The method of claim 38, wherein the database is included in a computer-readable medium.

40. The method of claim 39, wherein the database is in communications with a microprocessor and microprocessor instructions for providing a user interface to receive expression level data of a subject and to compare the expression level data with the database.

41. A method for determining the effectiveness of a treatment intended to reduce bone or cartilage formation, comprising obtaining a biological sample from the subject and comparing gene expression levels in the biological sample to those of a set of reference levels of expression during normal bone and cartilage formation, wherein significant differences in the levels of expression of the plurality of genes indicates that the treatment is effective.

42. The method of claim 31, comprising

obtaining a patient sample from a caregiver;

identifying expression levels of a plurality of genes listed in Table 1, 2, 5 and/or 6 from the patient sample;

determining whether the levels of expression of the genes in the patient sample are more similar to those of a cell differentiating into bone or cartilage or to those of a precursor cell; and

transmitting the results to the caregiver.

43. The method of claim 42, wherein the results are transmitted across a network.

44. A method for identifying a compound for treating a disease related to bone or cartilage formation, comprising

providing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a cell of a subject incubated with a test compound;

providing levels of expression of a cell differentiating into bone or cartilage; and

comparing the two levels of expression,

wherein significantly different levels of expression in the two cells indicates that the compound is likely to be effective for treating a disease related to bone or cartilage formation.

45. A method for identifying a compound for treating a disease related to bone or cartilage resorption, comprising

providing levels of expression of a plurality of genes listed in Table 1, 2, 5 and/or 6 in a cell of a subject incubated with a test compound;

providing levels of expression of a cell differentiating into bone or cartilage; and

comparing the two levels of expression,

wherein significantly similar levels of expression in the two cells indicates that the compound is likely to be effective for treating a disease related to bone or cartilage formation.

46. A method for identifying a compound that modulates bone or cartilage formation, comprising

contacting a mesenchymal precursor cell with an agent that stimulates bone or cartilage formation and a test compound; and

determining the level of expression of one or more genes of Tables 1, 2, 6 and 7 during the bone or cartilage formation;

wherein a significant similarity or difference between the expression level of the genes in the cell and reference expression levels of the genes during bone or cartilage formation indicates that the test compound modulates bone or cartilage formation.

47. The method of claim 46, wherein the reference expression levels are essentially identical to the levels set forth in Table 1, 2, 5 and/or 6.

48. A method for identifying a compound that stimulates bone or cartilage formation, comprising

contacting a mesenchymal precursor cell with a test compound; and

determining the level of expression of one or more genes of Tables 1, 2, 6 and 7 in the cell over time;

wherein a similarity between the expression level of the genes in the cell and reference expression levels of the genes during bone or cartilage formation indicates that the test compound stimulates bone or cartilage formation.

49. The method of claim 48, wherein the reference expression levels are levels set forth in Table 1, 2, 5 and/or 6.

50. A method for identifying a compound that binds to a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6, comprising

contacting a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6 with a test compound under essentially physiological conditions; and

determining whether the compund binds to the polypeptide;

51. A method for identifying a compound that modulates a biological activity of a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6, comprising

contacting a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6 with a test compound under essentially physiological conditions; and

determining the biological activity of the polypeptide,

wherein a higher or lower biological activity of the polypeptide in the presence of the test compound relative to the absence of the test compound indicates that the test compound modulates the biological activity of the polypeptide.

52. The method of claim 51, wherein the gene is CLF-1 or MMP23.

53. A method for identifying a compound for treating a disease related to bone or cartilage formation or resorption, comprising

identifying a compound that modulates the activity of a polypeptide encoded by a gene listed in Table 1, 2, 6 or 7 according to the method of claim 51; and

contacting a mesenchymal precursor cell with the compound in the presence or absence of an agent that stimulates the differentiation into bone or cartilage,

wherein stimulation or inhibition of bone or cartilage formation from the mesenchymal cell indicates that the test compound is effective for treating a disease related to bone or cartilage formation or resorption.

54. A method for treating a disease related to bone or cartilage formation or resorption, comprising administering to a subject having a disease related to bone or cartilage formation or resorption a compound that modulates the biological activity of a polypeptide encoded by a gene listed in Table 1, 2, 5 and/or 6 and thereby modulates bone or cartilage formation, to thereby treat the disease in the subject.

55. A diagnostic or drug discovery kit, comprising a computer-readable medium of claim 1 and instructions for use.

56. A diagnostic or drug discovery kit, comprising a composition of claim 11 and instructions for use.

57. A diagnostic or drug discovery kit, comprising a solid surface of claim 17 and instructions for use.

Figure 1

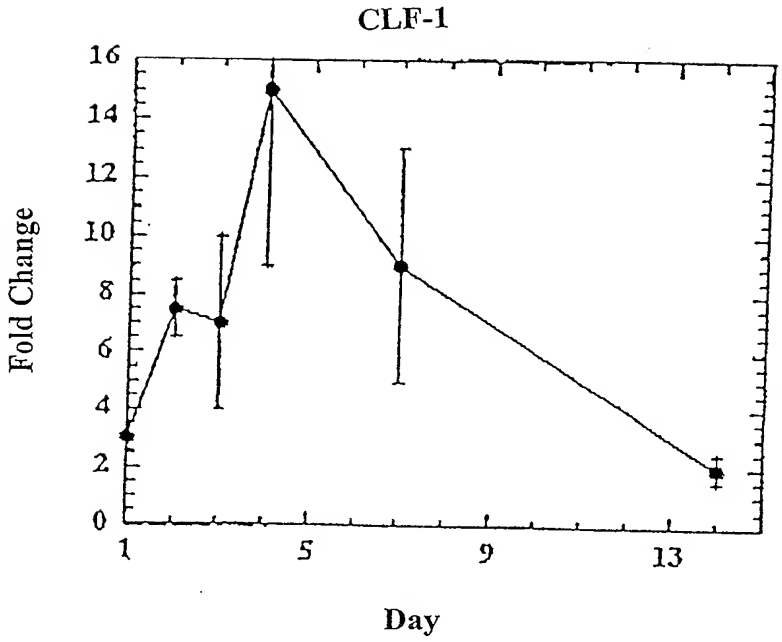
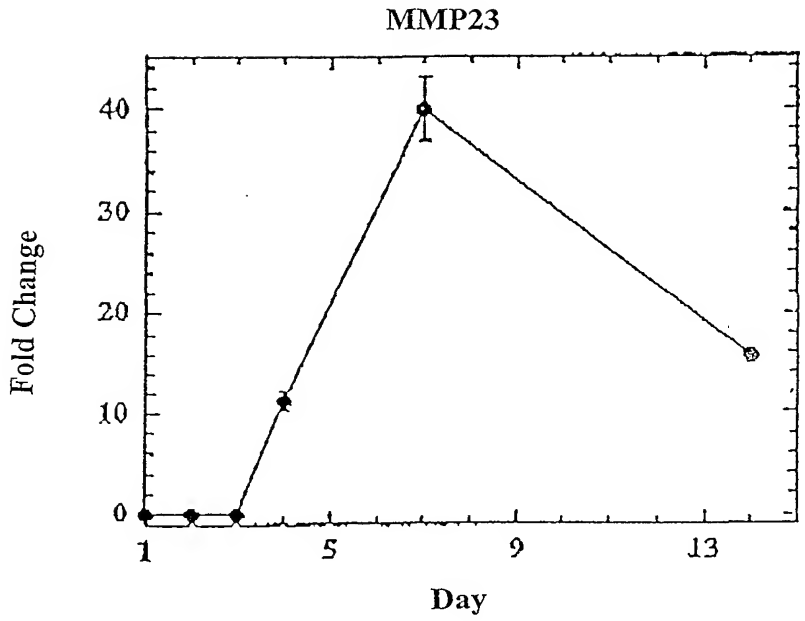


Figure 2



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Ala Arg Gly Pro Ala Arg
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Ile Leu Ser Phe Pro Arg Asn Leu Leu Ser Pro Arg Glu Thr Arg Arg
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Glu Ala His Leu Ser Ile Ile Ala Asn Ala Val Asn Glu Gly Thr Tyr
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Thr Cys Val Val Arg Arg Gln Gln Arg Val Leu Thr Thr Tyr Ser Trp
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Arg Val Arg Val Arg Gly
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Published:
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(88) Date of publication of the international search report:
20 March 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/085285 A3

(54) Title: METHODS AND REAGENTS FOR REGULATING BONE AND CARTILAGE FORMATION

(57) Abstract: The invention provides methods and compositions for diagnostic assays for detecting bone and cartilage formation and therapeutic methods and compositions for treating disease and disorders related to bone and cartilage formation or resorption, such as osteoporosis and bone fractions. The invention also provides therapeutic methods for diseases related to bone or cartilage formation or resorption. Methods for identifying therapeutics for such diseases are also provided.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US02/12149

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :G06F 7/06,17/30

US CL : 707/102, 104.1; 345/521

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 707/102, 104.1; 345/521

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN in line

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,966,711 A (ADAMS) 12 October 1999, claims 1, 13	1-10
Y	WO 99/05323 A1 (AFFYMETRIX) 04 February 1999, claims 1-27.	1-10
Y	Database Caplus, DN 133:84852, VAN STEENSELl et al. Probing the Gene expression Database for candidate genes. European Journal of Human Genetics. 1999, Vol. 7, No. 8, pp. 910-919	1-10
Y	Datbase GenBank, Accession Number AB040038, Mus Musculus CRLM3 mRNA for Cytokine Receptor like Molecule 3, complete cds. 16 March 2000.	1-10

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

11 OCTOBER 2002

Date of mailing of the international search report

19 DEC 2002

Name and mailing address of the ISA/US
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Form PCT/ISA/210 (second sheet) (July 1998)★

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US02/12149

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-10

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US02/12149

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

Group I, claims 1-10, drawn to a computer-readable medium, computer system and computer program.
Group II, claims 11-19, drawn to composition comprising a plurality of detection agents of genes.
Group III, claims 20-21, drawn to composition comprising a plurality of antagonists.
Group IV, claim 22, drawn to composition comprising a plurality of agonists.
Group V, claims 23-30, drawn to method for determining differences between levels of expression of genes.
Group VI, claims 31,32,42,43 drawn to method for determining whether a subject is likely to develop a bone resorption disease.
Group VII, claims 33-41 drawn to method for determining whether a subject is likely to develop a bone formation disease and evaluating the effectiveness of treatment.
Group VIII, claims 44-49 drawn to method for identifying compounds for treatment bone disease, said method based on gene. Group IX, claim 50, drawn to method for identifying compounds that bind to polypeptides.
Group X, claim 51,52 drawn to method for identifying compounds that modulate biological activity of a polypeptides.

The inventions listed as Groups I-IV do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features. A computer medium/system of Group I does not encompass compositions of detection agents, or agonists, or antagonists of Groups II-IV. Compositions of Groups II-IV do not have a common core structure required for a common utility. Methods of Groups II-IV do not utilize detection agents, or agonists, or antagonists, a computer system of Groups I-IV. Each of methods of Groups V-X claim a distinct and separate method (Group V - method for determining differences between levels of expression of genes; Group VI - method for determining whether a subject is likely to develop a bone resorption disease; Group VII - method for determining whether a subject is likely to develop a bone formation disease; Group VIII - method for identifying compounds for treatment bone disease, said method based on gene; Group IX -method for identifying compounds that bind to polypeptides; Group X - method for identifying compounds that modulate biological activity of a polypeptides). The methods do not share a special technical feature because each method contains specific and unique method steps which are not shared by each of the other methods and each method has a unique and distinct outcome. Thus, groups I-X do not share a corresponding special technical feature(s).